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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:04 ; Search time 20.73 Seconds

(Without alignments)  
144,928 Million cell updates/sec

Title: US-09-010-377-2  
Perfect score: 655  
Sequence: 1 QVQLVSGAVERKKPKASVKV.....NIGVYAMDYWGQGLTVTSS 123

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	123	2	US-08-561-521-11 Sequence 11, App1
2	655	100.0	123	5	PCT-US95-01219-11 Sequence 11, App1
3	655	100.0	142	2	US-08-561-521-17 Sequence 17, App1
4	655	100.0	142	5	PCT-US95-01219-17 Sequence 17, App1
5	552	84.3	123	2	US-08-561-521-9 Sequence 9, App1
6	552	84.3	123	5	PCT-US95-01219-9 Sequence 9, App1
7	544	83.1	140	2	US-08-561-521-4 Sequence 4, App1
8	544	83.1	140	5	PCT-US95-01219-4 Sequence 4, App1
9	523.5	79.9	117	4	US-08-871-488A-19 Sequence 19, App1
10	523	79.8	117	4	US-08-646-265A-132 Sequence 132, App
11	523	79.8	136	4	US-08-646-265A-99 Sequence 99, App
12	523	79.8	269	4	US-08-646-265A-109 Sequence 109, App
13	515	78.6	119	2	US-08-561-521-13 Sequence 13, App1
14	515	78.6	119	5	PCT-US95-01219-13 Sequence 13, App1
15	512	78.2	119	2	US-08-561-521-12 Sequence 12, App1
16	512	78.2	119	5	PCT-US95-01219-12 Sequence 12, App1
17	505	77.1	125	2	US-08-561-521-44 Sequence 44, App1
18	505	77.1	125	5	PCT-US95-01219-44 Sequence 44, App1
19	495	75.6	119	2	US-08-561-521-10 Sequence 10, App1
20	495	75.6	119	5	PCT-US95-01219-10 Sequence 10, App1
21	492	75.1	117	5	PCT-US95-10053-14 Sequence 17, App1
22	492	75.1	117	5	PCT-US95-10053-14 Sequence 17, App1
23	492	75.1	117	5	PCT-US96-09448-17 Sequence 17, App1
24	491.5	74.7	118	4	US-08-232-081B-8 Sequence 8, App1
25	489.5	74.7	120	4	US-08-025-769B-36 Sequence 36, App1
26	489.5	74.7	120	4	US-09-025-769B-59 Sequence 59, App1
27	486	74.2	140	3	US-08-836-561-63 Sequence 63, App1

28	484.5	74.0	135	1	US-08-137-117D-112 Sequence 112, App
29	484.5	74.0	135	2	US-08-436-717-112 Sequence 112, App
30	484.5	74.0	139	1	US-08-253-877C-19 Sequence 19, App1
31	484.5	74.0	139	2	US-08-452-164A-19 Sequence 19, App1
32	484.5	74.0	139	3	US-08-603-024-18 Sequence 18, App1
33	481	73.4	121	1	US-08-202-047-23 Sequence 23, App1
34	481	73.4	121	3	US-08-964-690-23 Sequence 23, App1
35	474	72.4	140	3	US-08-836-561-74 Sequence 74, App1
36	473	72.2	123	1	US-08-482-882-53 Sequence 53, App1
37	473	72.2	123	2	US-08-483-389-53 Sequence 53, App1
38	473	72.2	123	2	US-08-487-113D-53 Sequence 53, App1
39	473	72.2	123	2	US-08-473-503-53 Sequence 53, App1
40	473	72.2	123	2	US-08-483-932-53 Sequence 53, App1
41	473	72.2	123	2	US-08-720-420A-53 Sequence 53, App1
42	473	72.2	123	3	US-08-714-017-53 Sequence 53, App1
43	473	72.2	123	3	US-08-475-680-53 Sequence 53, App1
44	472	72.1	123	1	US-08-482-882-86 Sequence 86, App1
45	472	72.1	123	2	US-08-483-389-86 Sequence 86, App1

#### ALIGNMENTS

RESULT 1  
US-08-561-521-11  
Sequence 11 Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legier, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-11

Query Match 100.0%; Score 655; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1,8e-58;

Matches	123	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	QVQLVQSGAEVKKPCASVKVSCKASGFNFKDYYIMHWROAPQPLEMGRIPANGYTKY	60						
Db	1	QVQLVQSGAEVKKPCASVKVSCKASGFNFKDYYIMHWROAPQPLEMGRIPANGYTKY	60						
QY	61	DPKPGGRVITITADTSASTAYMELSLRSEDTAVYYCARREGYGGNGVYAMDYWGCGTLVT	120						
Db	61	DPKPGGRVITITADTSASTAYMELSLRSEDTAVYYCARREGYGGNGVYAMDYWGCGTLVT	120						
QY	121	VSS	123						
Db	121	VSS	123						

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1      RESULT      2
2      PCT-US95-01219-11
3      ; Sequence 11, Application PC/TUS9501219
4      ; GENERAL INFORMATION:
5      ; APPLICANT: Bendig, Mary M.
6      ; APPLICANT: Leger, Olivier J.
7      ; APPLICANT: Saldanha, Jose
8      ; APPLICANT: Jones, S. Tarian
9      ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
10     ; TITLE OF INVENTION: Adhesion Molecule VLA-4
11     ; NUMBER OF SEQUENCES: 45
12     ; CORRESPONDENCE ADDRESSES:
13     ; ADDRESSSEE: Townsend and Townsend Khourie and Crew
14     ; STREET: One Market Plaza, Steuart Tower, Suite 2000
15     ; CITY: San Francisco
16     ; STATE: California
17     ; COUNTRY: USA
18     ; ZIP: 94105
19     ;
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOS
24     ; SOFTWARE: Patent In Release #1.0, Version #1.25
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: PCT/US95/01219
27     ; FILING DATE: 25-JAN-1995
28     ;
29     ; CLASSIFICATION:
30     ; PRIOR APPLICATION DATA:
31     ; APPLICATION NUMBER: US 08/186,269
32     ; FILING DATE: 25-JAN-1994
33     ; ATTORNEY/AGENT INFORMATION:
34     ; NAME: Smith, William L.
35     ; REGISTRATION NUMBER: 30,223
36     ; REFERENCE/DOCKET NUMBER: 15270-14
37     ; TELECOMMUNICATION INFORMATION:
38     ; TELEPHONE: 415-543-9600
39     ; TELEFAX: 415-543-5043
40     ; INFORMATION FOR SEQ ID NO: 11:
41     ; SEQUENCE CHARACTERISTICS:
42     ; LENGTH: 123 amino acids
43     ; TYPE: amino acid
44     ; STRANDEDNESS: single
45     ; TOPOLOGY: linear
46     ; MOLECULE TYPE: protein
47     ;
48     ; PCT-US95-01219-11

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Query	Match	Similarity	100.0%	Score	655	DB	5	Length	123
Best	Local	Similarity	100.0%	Pred.	No.	1.8e-58			
Matches	123	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	QVQLVSGAEEVKKPKGASVYSCASGFENIKDITYIHVWRAPGGRLEPMGRIDPANGTKY	60						
Db	1	QVQLVSGAEEVKKPKGASVYSCASGFENIKDITYIHVWRAPGGRLEPMGRIDPANGTKY	60						
QY	61	DPKFGGRVITTTADFSASTAYMELSLRSSEDTAYYCARCEGYNNGVYADWDYGQGLT	120						
Db	61	DPKFGGRVITTTADFSASTAYMELSLRSSEDTAYYCARCEGYNNGVYADWDYGQGLT	120						

QY	121	VSS	123
Db	121	VSS	123

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1      RESULT      3
2      US-08-561-521-17
3      : Sequence 17, Application US/08561521
4      : Patent No. 5840299
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Bendig, Mary M.
9      : APPLICANT: Leger, Olivier J.
10     : APPLICANT: Saldaña, Jose
11     : APPLICANT: Jones, S. Tarran
12     : TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
13     : TITLE OF INVENTION: Adhesion Molecule VLA-4
14     : NUMBER OF SEQUENCES: 45
15     : CORRESPONDENCE ADDRESS:
16     : ADDRESS: Townsend and Townsend Hourie and Crew
17     : STREET: One Market Plaza, Steuart Tower, Suite 2000
18     : CITY: San Francisco
19     : STATE: California
20     : COUNTRY: USA
21     : ZIP: 94105
22     :
23     : COMPUTER READABLE FORM:
24     : MEDIUM TYPE: Floppy disk
25     : COMPUTER: IBM PC compatible
26     : OPERATING SYSTEM: PC-DOS/MS-DOS
27     : SOFTWARE: Patentn Release #1.0, Version #1.25
28     :
29     : CURRENT APPLICATION DATA:
30     : APPLICATION NUMBER: US/08/561,521
31     : FILING DATE:
32     : CLASSIFICATION: 424
33     :
34     : PRIOR APPLICATION DATA:
35     : APPLICATION NUMBER: US/08/186,269A
36     : FILING DATE: 25-JAN-1994
37     : ATTORNEY/AGENT INFORMATION:
38     : NAME: Smith, William L.
39     : REGISTRATION NUMBER: 30,223
40     : REFERENCE/DOCKET NUMBER: 15270-14
41     :
42     : TELECOMMUNICATION INFORMATION:
43     : TELEPHONE: 415-543-9600
44     : TELEFAX: 415-543-5043
45     : INFORMATION FOR SEQ ID NO: 17:
46     : SEQUENCE CHARACTERISTICS:
47     : LENGTH: 142 amino acids
48     : TYPE: amino acid
49     : TOPOLOGY: linear
50     :
51     : MOLECULE TYPE: protein
52     :
53     : US-08-561-521-17

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Query Match	Similarity	100.0%	Score	655:	DB 23	Length	142:
Best Local	Similarity	100.0%	Pred. No.	2.2e-56:			
Matches	123:	Conservative	0:	Mismatches	0:	Indels	0:
							Gaps
							0:
QY	1	QVOLVOSGAENVKPGASVYVSCKASGFNIKDYIHWVRQAPQORLEMMGRIDPANGYTKY	60				
Db	20	QVOLVOSGAENVKPGASVYVSCKASGFNIKDYIHWVRQAPQORLEMMGRIDPANGYTKY	79				
QY	61	DKPFGQGVITITADTASSTAYMELSLRSRSDTAYYTCARFGYTGNGVYAMDYWGQGLVT	120				
Db	80	DKPFGQGVITITADTASSTAYMELSLRSRSDTAYYTCARFGYTGNGVYAMDYWGQGLVT	139				
QY	121	VSS 123					
Db	140	VSS 142					

RESULT 4  
PCT-US95-01219-17  
; Sequence 17, Application PC/TUS9501219



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-9

Query Match Best Local Similarity 84.3%; Score 552; DB 5; Length 123;  
Matches 102; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKASCAGSFINIKDTYTHWVROAPGQRLPMGRIDPANGYTKY 60  
DB 1 EVQLQDSGAEIVKPGASVKSLCTASGFINIKDTYTHWVROAPGQRLPMGRIDPANGYTKY 60  
QY 61 DPKFGAVTTADTSASTAYMELSLRSEDTAVYYCARREGYGNVGVYAMDYGQGTLYT 120  
DB 61 DPKFGAVTTADTSASTAYMELSLRSEDTAVYYCARREGYGNVGVYAMDYGQGTLYT 120  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 7  
US-08-561-521-4  
Sequence 4, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legert, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269

FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-4

Query Match Best Local Similarity 83.1%; Score 544; DB 2; Length 140;  
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKASCAGSFINIKDTYTHWVROAPGQRLPMGRIDPANGYTKY 60  
DB 20 EVQLQDSGAEIVKPGASVKSLCTASGFINIKDTYTHWVROAPGQRLPMGRIDPANGYTKY 79  
QY 61 DPKFGAVTTADTSASTAYMELSLRSEDTAVYYCARREGYGNVGVYAMDYGQGTLYT 120  
DB 80 DPKFGAVTTADTSASTAYMELSLRSEDTAVYYCARREGYGNVGVYAMDYGQGTLYT 139  
QY 121 V 121  
DB 140 V 140

RESULT 8  
PCT-US95-01219-4  
Sequence 4, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legert, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:



Db 1 QVQLVDSGAEVKKPGSSVKASGPNIKDTYIHWRQAPGQGLEWMGRIDPADGNTKY 60  
QY 61 DPKFGGRVITITADTSASTAYMELSLRSEDPAVYVCARGGYGNVYANDYWGQGLT 120  
Db 61 DPKFGGRVITITADESTINTAYMELSLRSEDPAFYFCA-SAYYVN-----QDYWGQGLT 114  
QY 121 VSS 123  
Db 115 VSS 117

RESULT 11  
US-08-646-265A-99  
Sequence 99, Application US/08646265A  
Patent No. 6214973

GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshiniko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-99

Query Match 79.8%; Score 523; DB 4; Length 136;  
Best Local Similarity 83.7%; Pred. No. 3.1e-45;  
Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps 2;

QY 1 QVQLVDSGAEVKKPGSSVKASGPNIKDTYIHWRQAPGQGLEWMGRIDPADGNTKY 60  
Db 20 QVQLVDSGAEVKKPGSSVKASGPNIKDTYIHWRQAPGQGLEWMGRIDPADGNTKY 79  
QY 61 DPKFGGRVITITADTSASTAYMELSLRSEDPAVYVCARGGYGNVYANDYWGQGLT 120  
Db 80 DPKFGGRVITITADESTINTAYMELSLRSEDPAFYFCA-SAYYVN-----QDYWGQGLT 133

QY 121 VSS 123  
Db 134 VSS 136

RESULT 12  
US-08-646-265A-109  
Sequence 109, Application US/08646265A  
Patent No. 6214973

GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshiniko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-109

Query Match 79.8%; Score 523; DB 4; Length 269;  
Best Local Similarity 83.7%; Pred. No. 6.9e-45;  
Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps 2;

QY 1 QVQLVDSGAEVKKPGSSVKASGPNIKDTYIHWRQAPGQGLEWMGRIDPADGNTKY 60  
Db 23 QVQLVDSGAEVKKPGSSVKASGPNIKDTYIHWRQAPGQGLEWMGRIDPADGNTKY 82  
QY 61 DPKFGGRVITITADTSASTAYMELSLRSEDPAVYVCARGGYGNVYANDYWGQGLT 120  
Db 83 DPKFGGRVITITADESTINTAYMELSLRSEDPAFYFCA-SAYYVN-----QDYWGQGLT 136  
QY 121 VSS 123  
Db 137 VSS 139

RESULT 13

US-08-561-521-13  
Sequence 13, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-13

Query Match 78.6%; Score 515; DB 2; Length 119;  
Best Local Similarity 82.9%; Pred. No. 1.7e-44;  
Matches 102; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKASKASGFNIDYTIHWYRQAPGQRLWMGRIDPANGYTKY 60  
|||||  
Db 1 QVOLVSGAEVKKPGASVKASKASGFNIDYTIHWYRQAPGQRLWMGRIDPANGYTKY 60  
QY 61 DPKFGQGVTTADTSASTAYMELSLRSEDYAVYYCARREGYGNVGYADYWGQGLTVT 120  
|||||  
Db 61 SOKFGQGVTTADTSASTAYMELSLRSEDYAVYYCARREGYGNVGYADYWGQGLTVT 116  
QY 121 VSS 123  
|||  
Db 117 VSS 119

RESULT 14  
PCT-US95-01219-13  
Sequence 13, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-13

Query Match 78.6%; Score 515; DB 5; Length 119;  
Best Local Similarity 82.9%; Pred. No. 1.7e-44;  
Matches 102; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVKASKASGFNIDYTIHWYRQAPGQRLWMGRIDPANGYTKY 60  
|||||  
Db 1 QVOLVSGAEVKKPGASVKASKASGFNIDYTIHWYRQAPGQRLWMGRIDPANGYTKY 60  
QY 61 DPKFGQGVTTADTSASTAYMELSLRSEDYAVYYCARREGYGNVGYADYWGQGLTVT 120  
|||||  
Db 61 SOKFGQGVTTADTSASTAYMELSLRSEDYAVYYCARREGYGNVGYADYWGQGLTVT 116  
QY 121 VSS 123  
|||  
Db 117 VSS 119

RESULT 15  
US-08-561-521-12  
Sequence 12, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ. ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-12

Query Match 78.2%; Score 512; DB 2; Length 119;  
Best Local Similarity 82.9%; Pred. NO. 3.3e-44;  
Matches 102; Conservative 4; Mismatches 13; Indels 4; Gaps 1;  
QY 1 QVQLVQSGAEVKKPKQASVKYSCAKSGENIKDFTYIHWRQAPQRLWMGRIDPANGYTKY 60  
Db 1 QVQLVQSGAEVKKPKQASVKYSCAKSGENIKSYAMHWVROAPQGLEWMGWINAGNNTKY 60  
QY 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYTGNVGVYAMDYWGQGLVT 120  
Db 61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYGS---GSNYWGQGLVT 116  
QY 121 VSS 123  
Db 117 VSS 119

Search completed: July 9, 2002, 15:39:04  
Job time: 30 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2002, 15:38:34 ; Search time 28.27 Seconds  
(without alignments)  
360.293 Million cell updates/sec

Title: US-09-010-377-1

Perfect score: 562  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....YCLQYDNLMTFCGCTKVEIK 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 28338 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28338

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_71:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	86.8	104	2 S26330	Ig kappa chain V r
2	479	85.2	104	2 S26329	Ig kappa chain V r
3	478	85.1	106	2 C33936	Ig kappa chain V r
4	463.5	82.5	125	2 S09365	Ig kappa chain - m
5	452	80.4	97	2 PH1064	Ig light chain V r
6	446.5	79.4	107	2 PL0270	Ig kappa chain V r
7	443.5	78.9	108	1 K1HUR	Ig kappa chain V r
8	443.5	78.9	129	2 S52789	Ig kappa chain V r
9	443	78.8	103	2 S26332	Ig kappa chain V r
10	440.5	78.4	107	2 PL0272	Ig kappa chain V r
11	440	78.3	94	2 E33730	Ig kappa chain V r
12	439.5	78.2	107	2 PL0269	Ig kappa chain V r
13	439.5	78.2	107	2 PL0271	Ig kappa chain V r
14	439.5	78.2	108	1 K1HUR	Ig kappa chain V r
15	435.5	77.5	108	2 I39154	Ig kappa chain (BR
16	429.5	76.4	110	2 S44118	Ig kappa chain V-J
17	429.5	76.4	127	2 S40367	Ig kappa chain V-J
18	426	75.8	107	2 S36775	Ig kappa chain V-J
19	424.5	75.5	125	2 S40333	Ig kappa chain V-I
20	421.5	75.0	108	1 K1HUR	Ig kappa chain V-I
21	419.5	74.6	108	1 K1HUR	Ig kappa chain V-I
22	419.5	74.5	123	2 S40331	Ig kappa chain - h
23	418.5	73.9	109	2 S31998	Ig kappa chain V-J
24	415.5	73.8	131	2 S40332	Ig kappa chain V-J
25	414.5	73.7	124	2 S40336	Ig kappa chain V-J
26	414	73.6	108	1 K1HUR	Ig kappa chain V r
27	413.5	73.6	108	1 K1HUR	Ig kappa chain V r
28	412.5	73.3	106	2 PC2397	anti-tetanus toxin
29	412	73.3	106	2 PC2397	anti-tetanus toxin

30	410.5	73.0	108	2 S44122	Ig kappa chain V r
31	410.5	73.0	109	2 S31981	Ig kappa chain - h
32	409.5	72.9	129	1 K1HUR	Ig kappa chain pre
33	409	72.8	107	1 K1HUR	Ig kappa chain V-I
34	408.5	72.7	108	1 K1HUR	Ig kappa chain V-I
35	408.5	72.7	139	2 S40365	Ig kappa chain - h
36	407.5	72.5	141	2 S49134	Ig kappa chain V-I
37	405.5	72.2	117	2 S46371	Ig kappa chain V r
38	405	72.1	108	2 S30521	Ig kappa chain - h
39	404.5	72.0	132	2 S40334	Ig kappa chain V r
40	403.5	71.8	94	2 PH1063	Ig light chain V r
41	403.5	71.8	107	2 S36264	Ig kappa chain V r
42	403.5	71.8	127	2 S11240	Ig kappa chain V r
43	403	71.7	117	2 S43528	Ig kappa chain V r
44	403	71.7	117	2 S42263	Ig kappa chain V r
45	402.5	71.6	108	1 K1HUR	Ig kappa chain V-I

## ALIGNMENTS

RESULT 1  
S26330  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26330  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protei  
A:Reference number: S26309; MUID:91341421  
A:Accession: S26330  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-104 <STA>  
A:Cross-references: EMBL:X59185; NID:952316; PIRN:CA441895.1; PID:91334063  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
P:16-90/Domain: immunoglobulin homology <IMV>

Query Match 86.8%; Score 488; DB 2; Length 104;  
Best Local Similarity 85.6%; Pred. No. 1.6e-35;  
Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKTSODINKYMANVQOTPKAPRLLIHYTSALQPGIPS 60  
|||||  
Db 1 DIQMTQSPSSLSASVGRVTITCKTSODINKYMANVQOTPKAPRLLIHYTSALQPGIPS 60  
QY 61 RFSGSGGRDYFTISLQPEDYATYYCLQYDNLMTFCGCTKVE 104  
|||||  
Db 61 RFSGSGGRDYFTISLQPEDYATYYCLQYDNLMTFCGCTKLE 104

RESULT 2  
S26329  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26329  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protei  
A:Reference number: S26309; MUID:91341421  
A:Accession: S26329  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-104 <STA>  
A:Cross-references: EMBL:X59173; NID:952309; PIRN:CA441883.1; PID:91334059  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
P:16-90/Domain: immunoglobulin homology <IMV>

Query Match	85.28;	Score 479;	DB 2;	Length 104;
Best Local Similarity	84.68;	Pred. No. 9.7e-35;		
Matches 88; Conservative		9; Mismatches 7;		Indels

QY 1 DIOMTSPSSLSASVGDVYITCTCKTSODINKMYAMWOOTPKKAPRLIIHTYSALGQIPS 60  
 ||||| ||||| : ||||| ||||| ||||| || || ||||| ||||| |||||  
 Db 1 DIOMTSPSSLSASLGKVTITCKASODINKYIAMYOHKPKGPRLLIHTYSLGQIPS 60

### RESULT 3

19\_kappa\_chan region (VM13) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000  
C/Accession: C33936  
R.Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989  
A>Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene  
A/Reference number: A33936; MUID:6920831  
A/Accession: C33936

QY 1 DIQMTSPSSLSASVGDRTITCKIKSODINKMYMYOOTPGKAPRLIIHTYSALQGPS 60  
|||||  
1 DIQMTSPSSLSASLGKGVITCKASODINKMYMYOHKPGKGRLLIHTYSALQGPS 60  
|||||

#### RESULT 4

Ig kappa chain mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
 C:Accession: S09365  
 R:Reddersen, R.; van Ness, B.  
 Nucleic Acids Res. 17, 9797-9809, 1989  
 A:Title: Direct evidence for intrastand DNA inversion of kappa immunoglobulin gene segm  
 A:Reference number: S09365; MUID:90098844  
 A:Accession: S09365  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-125 <FED>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:33-107/Domain: immunoglobulin homology <IMK>

Query Match	82.5%;	Score 463.5;	DB 2;	Length 125;
Best Local Similarity	83.2%;	Pred. No. 2.5e-33;		
Matches	89;	Conservative	7;	Mismatches 10;
				Indels 1.
				Gap 1.

**D**

QY 18	↓	Db
1		66
DIOMTSPSSLSASGVDRVTITCKTSODINKMYAMWYOOTPGKAPRLIHYSALQGIPS		77
DIOMTSPSSLSASLGKVITTCASODINKYIAMYOHKPGKPRLLIHTSTLQGIPS		77

```
QY 61 RFGSGSGRDTFTTISLPEDATYYCLOYNLW-TFGGKTVEIK 106
      |||||  ||: ||: ||||| |||||  || |||||
Db 78 RFGSGSGSDYSFISNLGPEDATYYCLOYNLLRTFGGKTLEIK 124
```

RESULT 5  
PH1.064

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH1064  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-97 <TTL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match	80.4%;	Score 452;	DB 2;	Length 97;
Best Local Similarity	85.68;	Pred. No. 1.9e-32;		
Matches	83;	Conservative	8;	Mismatches 6;
			Indels	0;
			Gaps	0;

[illegible]

RESULT	6
PI.0270	

Ig: kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 C:Accession: P10270  
 R:Shlomchik, M.; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat  
 A:Reference number: P10231; MUID:90111618  
 A:Accession: P10270  
 A:Molecule type: mRNA  
 A:Residues: 1-107 (SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-33/Region: framework 1  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:24-34/Region: complementarity-determining 1  
 F:35-49/Region: framework 2  
 F:50-56/Region: complementarity-determining 2  
 F:57-88/Region: framework 3  
 F:89-97/Region: complementarity-determining 3  
 F:98-107/Region: framework 4

Query Match	79.48;	Score 446.5;	DB 2;	Length 107;
Best Local Similarity	79.48;	Pred. No. 6.4e-32;		
Matches	85;	Conservative	11;	Mismatches 10;
			Indels	1;
			Gaps	1

```
QY 1 DIOWTSPSSLKASVDRYTIICCKTSODINKMYMYOQPEKAPRLIHTYSLAQGIPS 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DQ 1 DIOWTSPSSLKASLGDYTIICCKTSODINKMYMYOQPEKAPRLIHTYSLAQGIPS 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 RFGSGSGRDYPTTISLQPEDIAIYYLQDNL-WTFGGGTKEIK 106
```

Db 61 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 107

## RESULT 7

KIHURE

Ig kappa chain V-1 region (Rel) - human (tentative sequence)

C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000  
C:Accession: A91663; A01873  
R:Palin, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975  
A:Title: Die Primärstruktur einer Kistallinen monoklonalen Immunoglobulin-L-Kette vom K  
vollständigen Antikörpersequenz des Proteins.  
A:Reference number: A91663; MUID:76023758  
A:Accession: A91663  
A:Molecule type: protein  
A:Residues: 1-108 <PAL>  
A:Note: the C region of this chain has the Inv (1.2) marker  
R:Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protei  
Biochemistry 14, 4943-4952, 1975  
A:Title: The molecular structure of a dimer composed of the variable portions of the Ber  
A:Reference number: A90392; MUID:76039968  
A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
F:15-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status experimental

Query Match 78.9%; Score 443.5; DB 1; Length 108;  
Best Local Similarity 81.1%; Pred. No. 1.2e-31;

Matches 86; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIOMTOSPSLSASVGDVYITTCCTSDINKYAMYOOTPGKAPRLLIHYTSALOPGIPS 60  
Db 1 DIOMTOSPSLSASVGDVYITTCCTSDINKYAMYOOTPGKAPRLLIHYTSALOPGIPS 60

QY 61 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 105  
Db 61 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 106

## RESULT 8

S52789

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S52789  
R:Rocca, A.; Khamilich, A.A.; Touchard, G.; Mougencot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A:Reference number: S52789  
A:Accession: S52789  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: EMBL:X85995; NID:9758588; PIDN:CA55997.1; PID:9758589  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 78.9%; Score 443.5; DB 2; Length 129;  
Best Local Similarity 79.4%; Pred. No. 1.4e-31;  
Matches 85; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

QY 1 DIOMTOSPSLSASVGDVYITTCCTSDINKYAMYOOTPGKAPRLLIHYTSALOPGIPS 60

Db 23 DIOMTOSPSLSASVGDVYITTCCTSDINKYAMYOOTPGKAPRLLIHYTSALOPGIPS 82

QY 61 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 106  
Db 83 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 129

## RESULT 9

S26332

Ig light chain V region - mouse (fragment)

N:Alternate names: Ig kappa chain V region  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 20-Jun-2000  
C:Accession: S26332; S26331  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protei  
A:Reference number: S26309; MUID:91341421  
A:Accession: S26332  
A:Molecule type: mRNA  
A:Residues: 1-103 <STA>  
A:Cross-references: EMBL:X59187; NID:9523218; PIDN:CAA41897.1; PID:91334064  
A:Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are  
A:Accession: S26331  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-103 <STA>  
A:Cross-references: EMBL:X59191; NID:952321; PIDN:CAA41901.1; PID:91334066  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-90/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 443; DB 2; Length 103;  
Best Local Similarity 77.7%; Pred. No. 1.2e-31;

Matches 80; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDVYITTCCTSDINKYAMYOOTPGKAPRLLIHYTSALOPGIPS 60  
Db 1 DIOMTOSPSLSASVGDVYITTCCTSDINKYAMYOOTPGKAPRLLIHYTSALOPGIPS 60

QY 61 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 103  
Db 61 RFGSGSGRDYFSTISNLEPEDATYTCLODYKVPYFGSGTKLEIK 103

## RESULT 10

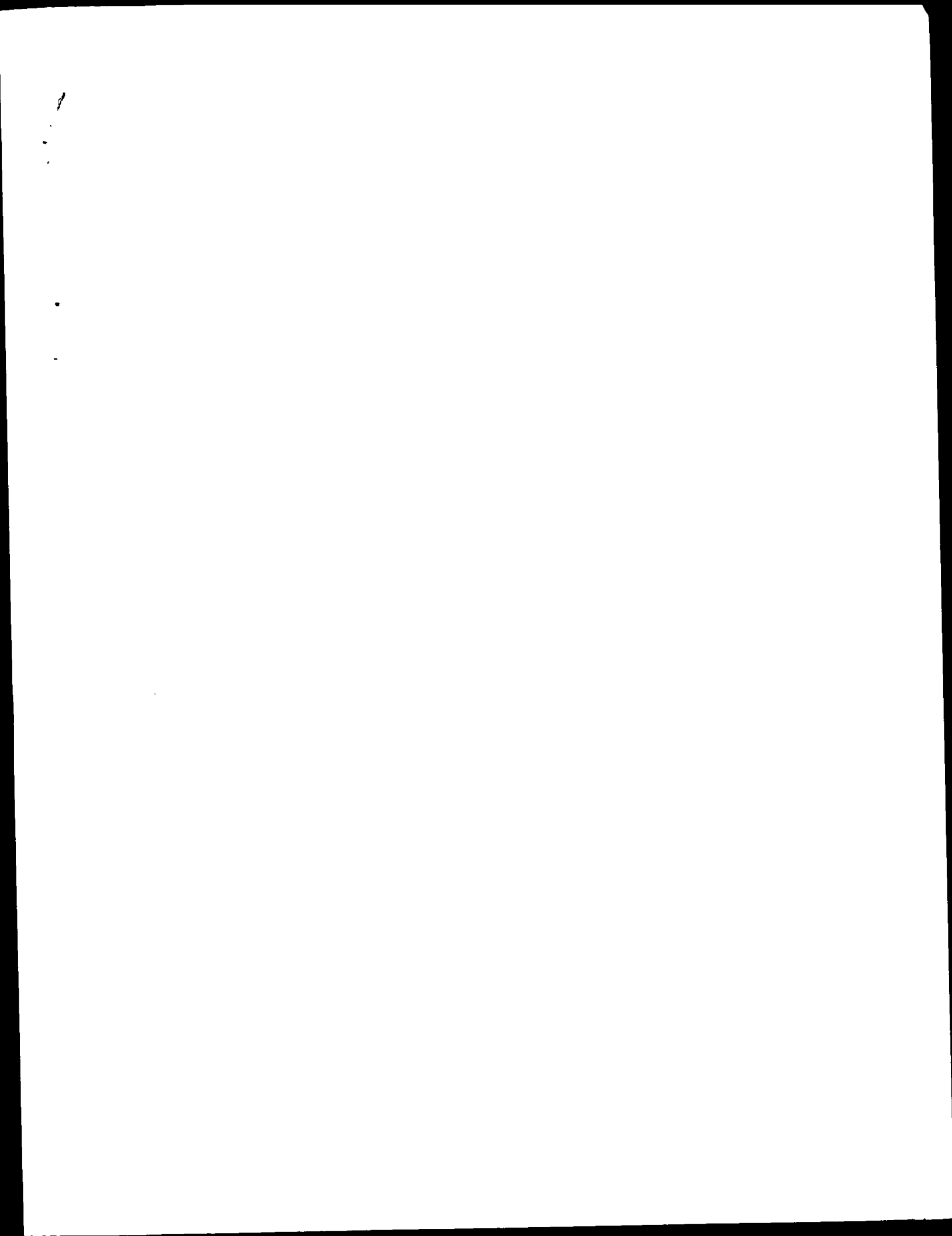
PL0272

Ig kappa chain V region (anti-DNA, 688VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C:Accession: PL0272  
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Piseraky, D.; Marshak-Rothstein  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat  
A:Reference number: PL0231; MUID:90111618  
A:Accession: PL0272  
A:Molecule type: mRNA  
A:Residues: 1-107 <SHL>  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1  
F:15-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2  
F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-107/Region: framework 4







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:44 ; Search time 15.81 Seconds

(Without alignments)  
259,600 Million Cell updates/sec

Title: US-09-010-377-1  
Perfect score: 562  
Sequence: 1 DIOMTOSPSLSASVGDRT.....YCLQYDNLMTGQTKVEIK 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	443.5	78.9	108	1	KV1O_HUMAN
2	439.5	78.2	108	1	KV1B_HUMAN
3	421.5	75.0	108	1	KV1M_HUMAN
4	419.5	74.6	108	1	KV1A_HUMAN
5	419.5	74.6	108	1	KV1P_HUMAN
6	419.5	74.6	108	1	KV1Y_HUMAN
7	413.5	73.6	108	1	KV1Q_HUMAN
8	409.5	72.9	129	1	KV1W_HUMAN
9	409	72.8	107	1	KVID_HUMAN
10	408.5	72.7	108	1	KV1R_HUMAN
11	402.5	71.6	108	1	KV1H_HUMAN
12	397.5	70.7	108	1	KV1F_HUMAN
13	396.5	70.6	108	1	KV1V_HUMAN
14	390.5	69.5	108	1	KV1K_HUMAN
15	388.5	69.1	108	1	KV1E_HUMAN
16	386.5	68.8	108	1	KV1L_HUMAN
17	385.5	68.6	108	1	KV1N_HUMAN
18	384.5	68.4	108	1	KV1C_HUMAN
19	383.5	68.2	108	1	KV1X_HUMAN
20	383.5	68.2	129	1	KV1G_HUMAN
21	381.5	67.9	108	1	KV1S_HUMAN
22	376.5	67.0	134	1	KV4C_HUMAN
23	371.5	66.1	108	1	KV5J_MOUSE
24	368	65.5	117	1	KV1J_HUMAN
25	366.5	65.2	128	1	KV5E_MOUSE
26	365	64.9	133	1	KV4B_HUMAN
27	364.5	64.9	108	1	KV5O_MOUSE
28	363.5	64.7	108	1	KV5N_MOUSE
29	362	64.4	109	1	KV1T_HUMAN
30	362	64.4	117	1	KV1I_HUMAN
31	361.5	64.3	108	1	KV5K_MOUSE
32	359.5	64.0	108	1	KV5M_MOUSE
33	358.5	63.8	108	1	KV5L_MOUSE

34	356.5	63.4	112	1	KV1U_HUMAN	P01613	homo	sapien
35	348.5	62.0	114	1	KV4A_HUMAN	P01625	homo	sapien
36	348	61.9	129	1	KV3H_HUMAN	P04207	homo	sapien
37	346	61.6	129	1	KV3M_HUMAN	P18136	homo	sapien
38	345.5	61.5	108	1	KV5T_MOUSE	P01653	mus	musculu
39	345	61.4	115	1	KV5F_MOUSE	P01638	mus	musculu
40	341.5	60.8	108	1	KV5O_MOUSE	P01650	mus	musculu
41	341	60.7	109	1	KV3E_HUMAN	P01623	homo	sapien
42	340.5	60.6	108	1	KV5S_MOUSE	P01652	mus	musculu
43	339.5	60.4	108	1	KV5U_MOUSE	P04946	mus	musculu
44	339	60.3	109	1	KV3D_HUMAN	P01622	homo	sapien
45	339	60.3	109	1	KV3F_HUMAN	P01624	homo	sapien

## ALIGNMENTS

RESULT 1  
KV1O\_HUMAN STANDARD: PRT: 108 AA.  
ID KV1O\_HUMAN  
AC P01607;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 19 kappa chain V-I region Rel.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76023758; PubMed=809329;  
RA Palm W., Hilschmann N.;  
RT "The primary structure of a crystal-line monoclonal immunoglobulin  
kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation  
and characterization of the tryptic peptides; the complete amino acid  
sequence of the protein; a contribution to the elucidation of the  
three-dimensional structure of antibodies. In particular their  
combining site.";  
RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
RL [2]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=76039968; PubMed=1182131;  
RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;  
RT "The molecular structure of a dimer composed of the variable portions  
of the Bence-Jones protein REI refined at 2.0-A resolution.";  
CC Biochemistry 14:4943-4952(1975).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
MARKER  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01873; KIHORE.  
DR PDB: 1REI; 17-FEB-84.  
DR InterPro: IPR003006; 19-MHC.  
DR InterPro: IPR003596; 19-V.  
DR Pfam: PF00047; 19; 1.  
DR SMART: SM00406; 19; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT STRAND 4 7  
FT STRAND 10 13  
FT TURN 15 16  
FT TURN 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 45 49

FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 85 90  
 FT STRAND 98 98  
 FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 78.9%; Score 443.5; DB 1; Length 108;  
 Best Local Similarity 81.1%; Pred. No. 5,9e-40;  
 Matches 86; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDRTITCKTSODINKYAMAYOOTPGKAPRLLIHYTSALOPGIPS 60  
 DB 1 DIOMTOSPSLSASVGDRTITCKTSODINKYAMAYOOTPGKAPRLLIHYTSALOPGIPS 60  
 OY 61 RFSGSGSGRDYFTFTISSLOPEDIAITYCQYDNLWTFGQGTVEIK 105  
 DB 61 RFSGSGSGRDYFTFTISSLOPEDIAITYCQYDNLWTFGQGTVEIK 106

## RESULT 2

KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schleich H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 protein Au).";  
 RT Hope-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RN [2]

RX X-RAY CRYSTALLOGRAPHY.  
 RP MEDLINE=77022433; PubMed=1234024;  
 RA Fehnamer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RT "The structure determination of the variable portion of the  
 Bence-Jones protein Au.";  
 RT Biophys. Struct. Mech. 1:139-146(1975).

CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 REGION OF THE KAPPA CHAIN REI.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR HSP: P01607; 1RET.  
 DR InterPro: IPR003596; 1G\_MHC.  
 DR Pfam: PF00047; 1G\_V.  
 DR SMART: SM00406; 1G\_V.  
 DR Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFD 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11939 MW; E801187EE6F89 CRC64;

Query Match 78.2%; Score 439.5; DB 1; Length 108;  
 Best Local Similarity 79.4%; Pred. No. 1.5e-39;  
 Matches 85; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDRTITCKTSODINKYAMAYOOTPGKAPRLLIHYTSALOPGIPS 60  
 DB 1 DIOMTOSPSLSASVGDRTITCKTSODINKYAMAYOOTPGKAPRLLIHYTSALOPGIPS 60  
 OY 61 RFSGSGSGRDYFTFTISSLOPEDIAITYCQYDNLWTFGQGTVEIK 106  
 DB 61 RFSGSGSGRDYFTFTISSLOPEDIAITYCQYDNLWTFGQGTVEIK 107

## RESULT 3

KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01605;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77038198; PubMed=824717;  
 RA Capra J.D., Klapper D.G.;  
 RT "Complete amino acid sequence of the variable domains of two human  
 IgM anti-gamma globulins (Lay/Pom) with shared idiotypic  
 specificities.";  
 RT Scand. J. Immunol. 5:677-684(1976).

CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS  
 CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN PGM V-II KAPPA CHAIN,  
 WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 GLOBULIN ACTIVITY.

DR HSP: P01607; 1RET.  
 DR InterPro: IPR003596; 1G\_MHC.  
 DR Pfam: PF00047; 1G\_V.  
 DR SMART: SM00406; 1G\_V.  
 DR Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFD 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 75.0%; Score 421.5; DB 1; Length 108;  
 Best Local Similarity 75.0%; Pred. No. 1.2e-37;  
 Matches 81; Conservative 11; Mismatches 13; Indels 3; Gaps 2;

OY 1 DIOMTOSPSLSASVGDRTITCKTSODINKYAMAYOOTPGKAPRLLIHYTSALOPGIPS 60  
 DB 1 DIOMTOSPSLSASVGDRTITCKTSODINKYAMAYOOTPGKAPRLLIHYTSALOPGIPS 60  
 OY 61 RFSGSGSGRDYFTFTISSLOPEDIAITYCQYDNLWTFGQGTVEIK 106



Db	61	RFSGSGSGDFPTFTISLQPEDIAATYVCOQVYNN-MPPFGCGTKVEVK	107
		1:      11:1 1:      1:1	
RESULT 4			
KV1A_HUMAN	STANDARD:	PRT:	108 AA.
AC P01593:			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE 19 kappa chain V-I region AG.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
SEQUENCE.			
RP MEDLINE=69234734; PubMed=4893682;			
RA Tiliari K., Shihoda T., Putnam F.W.;			
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The			
RL complete sequence and the location of the disulfide bridges.*"			
RL J. Biol. Chem. 244:3550-3560(1969).			
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.			
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR PIR: A01861; K1HDAG.			
DR HSSP: P01607; 1RE1.			
DR InterPro: IPR003006; 19_MHC.			
DR InterPro: IPR003596; 19_V.			
DR Pfam: PF00047; 19_1.			
DR SMART: SM00406; 19v_1.			
DR KW Immunoglobulin V region; Bence-Jones protein.			
FT DOMAIN 1 23 FRAMEWORK-1.			
FT FT 24 34 COMPLEMENTARITY-DETERMINING-1.			
FT DOMAIN 35 49 FRAMEWORK-2.			
FT FT 50 56 COMPLEMENTARITY-DETERMINING-2.			
FT DOMAIN 57 88 FRAMEWORK-3.			
FT FT 89 97 COMPLEMENTARITY-DETERMINING-3.			
FT DOMAIN 98 107 FRAMEWORK-4.			
FT DISULFID 23 88			
FT NON_TER 108 108			
SO SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CMC64;			
Query Match 74.6%; Score 419.5; DB 1; Length 108;			
Best Local Similarity 76.6%; Pred. No. 2e-37;			
Matches 82; Conservative 9; Mismatches 15; Indels 1; Gaps 1;			
OY 1 DIOMQSPSSLSASVSGDVTITCKTSQDINKMAYVQOTPGKAPRLIHYSALQPGIFS 60			
Db 1 DIOMQSPSSLSASVSGDVTITCKTSQDINKMAYVQOTPGKAPRLIHYSALQPGIFS 60			
OY 61 RFSGSGSGRDYFTFTISLQPEDIAATYVCOQVYNN-MPPFGCGTKVEIK 106			
Db 61 RFSGSGSGDFPTFTISLQPEDIAATYVCOQVYNN-MPPFGCGTKVEIK 107			
RESULT 5			
KV1P_HUMAN	STANDARD:	PRT:	108 AA.
AC P01608:			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE 19 kappa chain V-I region KY.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
SEQUENCE.			
RP MEDLINE=68362076; PubMed=5595110;			
RA Hilschmann N.;			

RT	CM	"Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";
RL	HL	Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN	12	
RP	REV	REVIEWS TO 39 AND 41.
RA	HL	Hiltschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Stelmeyer-Kayne M., Suter L., Matsubae S.;
RL	RL	(in) Erneek F., Shugart D. (eds.);
RL	RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
CC	-1	MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC	MARKER.	
CC	-1	MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR	PIR:	A01874; KIHURY.
DR	HSSP:	P80362; 1WTL.
DR	InterPro:	IPR003006; Ig_MHC.
DR	InterPro:	IPR003596; Ig_V.
DR	Pfam:	PF00047; 1g; 1.
DR	SMART:	SM00406; 1Gv; 1.
KW	Immunoglobulin V region:	Bence-Jones protein.
FT	DOMAIN	1 23 FRAMEWORK-1.
FT	FT	DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT	FT	DOMAIN 35 49 FRAMEWORK-2.
FT	FT	DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT	FT	DOMAIN 57 88 FRAMEWORK-3.
FT	FT	DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT	FT	DOMAIN 98 107 FRAMEWORK-4.
FT	FT	DISULFID 23 88 BY SIMILARITY.
FT	NON_TER	108 108
SO	SEQUENCE	108 AA; 11782 MW; F5ACDE5A313DF3A CRC64;
QY	Query Match	74.6%; Score 419.5; DB 1; Length 108;
Db	Best Local Similarity	75.7%; Pred. No. 2e-37;
Matches	81; Conservative	12; Mismatches 13; Indels 1; Caps
QY	1	DIDMTQSPSSLSASVGDRTYTRCTKTSIDINMYMYOOTPEKAPRLIHYTSALQGPIS 60
Db	1	DIDMTQSPSSLSASVGDRTYTRCTKTSIDINMYMYOOTPEKAPRLIHYTSALQGPIS 60
QY	61	RFGSGSGRDYPTFTTISLOPEDIAIYYCIQYDNL-WTFPGCGTKEIK 106
Db	61	RFGSGSGRDYPTFTTISLOPEDIAIYYCIQYDNL-WTFPGCGTKEIK 107
Db	61	RFGSGSGRDYPTFTTISLOPEDIAIYYCIQYDNL-WTFPGCGTKEIK 107
RESULT	6	
KV1Y	HUMAN	STANDARD; PRT; 108 AA.
AC	P80362;	
DT	01-NOV-1995 (Rel. 32, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig kappa chain V-1 region MAT.	
OS	Homo sapiens (Human).	
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	11	
RP	SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).	
RX	MEDLINE=95086080; PubMed=7993911;	
RA	Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M.;	
RT	"Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers";	
RL	Biochemistry 33:14848-14857(1994).	
RN	12	
RP	SEQUENCE OF 1-35.	
RX	MEDLINE=81267384; PubMed=6167731;	
RA	Stevens F.J., Westholm F.A., Pangiotopoulos N., Schiffer M., Popp R.A., Solomon A.;	
RT	"Characterization and preliminary crystallographic data on the VL-related fragment of the human kappa Bence Jones protein Wat.";	

BL J. Mol. Biol. 147:185-193(1981).  
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PDB: 1MTL; 01-NOV-94.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KM Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT CONFLICT 30 31  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match  
Best Local Similarity 74.6%; Score 419.5; DB 1; Length 108;  
Matches 81; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDVVTITCKTSODINKYMWYOOTPKAPRLLIHTYSALOPGIPS 60  
DB 1 DIOMTOSPSLSASVGDVVTITCKTSODINKYMWYOOTPKAPRLLIHTYSALOPGIPS 60  
OY 61 RSSGSGSGRDYFTTISLQPEDIAITYCLQYDNL-WTFGQGTKEIK 106  
DB 61 RSSGSGSGRDYFTTISLQPEDIAITYCLQYDNL-WTFGQGTKEIK 107

RESULT 7  
KV10\_HUMAN STANDARD; PRT; 108 AA.  
AC P01609;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 19 kappa chain V-I region Scw.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059271; PubMed=4435756;  
RA Eulitz M., Hilschmann N.;  
RT "The primary structure of a human immunoglobulin L-chain of  
RT kappa-type (Bence-Jones protein Scw.). II: The chymotryptic peptides  
RT and the complete amino acid sequence.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).  
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
CC MARKER.  
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01875; KIHUSW.  
DR HSSP: P01607; IPR1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KM Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

SO SEQUENCE 108 AA; 11764 MW; 32CECDDDE9644414 CRC64;

Query Match  
Best Local Similarity 73.6%; Score 413.5; DB 1; Length 108;  
Matches 80; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDVVTITCKTSODINKYMWYOOTPKAPRLLIHTYSALOPGIPS 60  
DB 1 DIOMTOSPSLSASVGDVVTITCKTSODINKYMWYOOTPKAPRLLIHTYSALOPGIPS 60  
OY 61 RSSGSGSGRDYFTTISLQPEDIAITYCLQYDNL-WTFGQGTKEIK 106  
DB 61 RSSGSGSGRDYFTTISLQPEDIAITYCLQYDNL-WTFGQGTKEIK 107

RESULT 8  
KV10\_HUMAN STANDARD; PRT; 129 AA.  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 19 kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA K1beck H.G., Combrato G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
RT lymphoid cell lines are closely related."  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC  
CC EMBL: X00965; CAZ5477.1; ALT\_TERM.  
DR PIR: A01883; KIHUWK.  
DR HSSP: P01607; IPR1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KM Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129  
FT DOMAIN 23 45  
FT DOMAIN 46 56  
FT DOMAIN 57 71  
FT DOMAIN 72 78  
FT DOMAIN 79 110  
FT DOMAIN 111 119  
FT DOMAIN 120 129  
FT DISULFID 45 110  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match  
Best Local Similarity 72.9%; Score 409.5; DB 1; Length 129;  
Matches 80; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDVVTITCKTSODINKYMWYOOTPKAPRLLIHTYSALOPGIPS 60  
DB 23 DIOMTOSPSLSASVGDVVTITCKTSODINKYMWYOOTPKAPRLLIHTYSALOPGIPS 82

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OY      61 RFSSGSGRDYFTFTISLOPEDATATVCLD-YDULMTFGCGTKEIK 106
          |||||||:|| ||||||| ||||| | |||||:||||
Db      83 RFSSGSGDTFTLTISLOPEDSATYYCOOSYSTLITFFGGTRLEIK 129

RESULT   9
KV_ID_HUMAN  ID        STANDARD;    PRT;     107 AA.
AC      P01596;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      19 kappa chain V-I region CAR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      MEDLINE=75075135; PubMed=4216454;
RA      Milstein C.P., Deverson E.V.;
RT      *Primary structure of kappa light chain from a human myeloma
RT      protein.*;
RL      Eur. J. Biochem. 49:377-391(1974);
CC      -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC      MARKER.
CC      -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR      HSP; P80362; IMLL.
DR      InterPro: IPR003006; IG_MHC.
DR      InterPro: IPR003596; IG-V.
DR      Pfam: PF00047; Ig: L.
DK      SMART: SM00406; IGV: 1.
KW      Immunoglobulin V region; Glycoprotein.
FT      CARDOHYD 28 28 N-LINKED (GLCNAC. . .).
FT      NON_TER 107 107
SQ      SEQUENCE 107 AA; 11703 MW; E1BFDPF9844C3346 CRC64;

Query Match           72.8%; Score 409; DB 1; Length 107;
Best Local Similarity 68.9%; Pred. No. 2.5e-36;
Matches 73; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

OY      1 DIOMTQSSPLASVGDYRVTTCSTKTSODINKIMAWYQQTPGRKAPRLIHYSLSALGPCPS 60
          |||||||:||||||| ||| :|||:||||| |||||:|:|:|:|:|
Db      1 DIOMTQSPSLASVGDYRAVITCRASONSISWLAAMYQOKRKAPKVLTKSSSLESQVPS 60

OY      61 RFSSGSGRDYFTFTISLOPEDATATVCLDYDNLMTFGCGTKEIK 106
          |||||||:| |||||:| ||||| ||| ||| |||||:|
Db      61 RFSSGSGDTFTLTISLZPBFRATYYCOQYNFFTFGPETKYDIK 106

RESULT 10
KV_ID_HUMAN  ID        STANDARD;    PRT;     108 AA.
AC      P01610;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      19 kappa chain V-I region MEA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      MEDLINE=83273707; PubMed=6410398;
RA      Conl F., Frangione B.;
RT      *Amino acid sequence of the Fv region of a human monoclonal IgM
RT      (protein MEA) with antibody activity against 3,4-pyruvylated
RT      galactose in Klebsiella polysaccharides K30 and K33.*;
RT      Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

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CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
CC AGAINST 3,4-PYRIDYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
CC WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR: A01876; KIHME.  
DR HSSP: PB0362; IHTL.  
DR InterPro: IPR003506; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam: PF00047; Iq; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Monoclonal antibody.

FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFD 23 88  
FT NON\_TER 108 108 BY SIMILARITY.

SQ SEQUENCE 108 AA: 11840 MW: 92496B10F9A5618C CRC64:

SO SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

## Query Match

Best Local Similarity 71.6%; Score 402.5; DB 1; Length 108;  
Matches 78; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 DIOMTOSPSLSASVGDRTITCKTSODINKYMAVYQOTPKAPRLIHYTSALOPGIPS 60  
DB 1 DIOMTOSPSLSASVGDRTITCKTSODINKYMAVYQOTPKAPRLIHYTSALOPGIPS 60  
QY 61 RFSGSGSGRDYFTTISLQPEDIAITYCLOVDNLMTFGGCKVEIK 106  
DB 61 RFSGSGSGTDFTLTITSLQPEDFATYVCOQVNSYRTTSGGCKVEIK 107

## RESULT 12

KYIF\_HUMAN STANDARD; PRT; 108 AA.

AC P01598;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE I9 kappa chain V-I region EU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
acid sequence of the light chain.";  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RX DISULFIDE BOND.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR: A01866; KIHUCU.  
DR HSSP: P01607; IRET.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR SMART: SM00406; IGV; 1.  
DR SMART: SM00406; IGV; 1.  
DR Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 2 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 3 35 49 FRAMEWORK-2.  
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 5 57 88 FRAMEWORK-3.  
FT DOMAIN 6 89 97 FRAMEWORK-4.  
FT DOMAIN 7 98 107 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SO SEQUENCE 108 AA; 11788 MW; 9CD294F2P4D88823 CRC64;

Query Match 70.7%; Score 397.5; DB 1; Length 108;  
Best Local Similarity 70.1%; Pred. No. 4e-35;

Matches 75; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

QY 1 DIOMTOSPSLSASVGDRTITCKTSODINKYMAVYQOTPKAPRLIHYTSALOPGIPS 60  
DB 1 DIOMTOSPSLSASVGDRTITCKTSODINKYMAVYQOTPKAPRLIHYTSALOPGIPS 60  
QY 61 RFSGSGSGRDYFTTISLQPEDIAITYCLOVDNLMTFGGCKVEIK 106  
DB 61 RFSGSGSGTDFTLTITSLQPEDFATYVCOQVNSYRTTSGGCKVEIK 107

DB 61 RFSGSGSGTEFTLTITSLQPEDFATYVCOQVNSDSKMEGCKVEIK 107

## RESULT 13

KYIV\_HUMAN STANDARD; PRT; 108 AA.

AC P04430;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE I9 kappa chain V-I region BAN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86174817; PubMed=3083240;  
RA Dwolet F.E., O'Connor T.P., Benson M.D.;  
RT "Polymorphism in a kappa I primary (Alu) amyloid protein (BAN).";  
RL Mol. Immunol. 23:73-78(1986).  
DR PIR: A01878; KIHUBN.  
DR HSSP: P80362; IWTU.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR SMART: SM00406; IGV; 1.  
DR SMART: SM00406; IGV; 1.  
DR Immunoglobulin V region; Amyloid.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 2 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 3 35 49 FRAMEWORK-2.  
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 5 57 88 FRAMEWORK-3.  
FT DOMAIN 6 89 97 FRAMEWORK-4.  
FT DOMAIN 7 98 107 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 23 88  
FT NON\_TER 108 108 BY SIMILARITY.  
SO SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 70.6%; Score 396.5; DB 1; Length 108;  
Best Local Similarity 70.1%; Pred. No. 5.1e-35;

Matches 75; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 DIOMTOSPSLSASVGDRTITCKTSODINKYMAVYQOTPKAPRLIHYTSALOPGIPS 60  
DB 1 DIOMTOSPSLSASVGDRTITCKTSODINKYMAVYQOTPKAPRLIHYTSALOPGIPS 60  
QY 61 RFSGSGSGRDYFTTISLQPEDIAITYCLOVDNLMTFGGCKVEIK 106  
DB 61 RFSGSGSGTDFTLTITSLQPEDFATYVCOQVNSYRTTSGGCKVEIK 107

## RESULT 14

KYIK\_HUMAN STANDARD; PRT; 108 AA.

AC P01603;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE I9 kappa chain V-I region Ka.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76189985; PubMed=818073;  
RA Shinoda T.;  
RT "Comparative structural studies on the light chains of human  
immunoglobulins. I. Protein Ka with the inv(3) allotypic marker.";  
RL J. Biochem. 77:1277-1296(1975).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
DR PIR: A01869: KIHUKA.  
DR HSSP: P80362: 1MTL.  
DR InterPro: IPR003006: 1g\_MHC.  
DR InterPro: IPR003596: 1g\_V.  
DR Pfam: PF00047: 1g: 1.  
DR SMART: SM00406: IGV: 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT 24 34 FRAMEWORK-1.  
FT 35 49 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 50 56 FRAMEWORK-2.  
FT 57 88 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 89 97 FRAMEWORK-3.  
FT 98 107 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 107 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11900 MW; 768839PBE5A2F4B CRC64;

Query Match 69.5%; Score 390.5; DB 1; Length 108;  
Best Local Similarity 66.4%; Pred. No. 2,2e-34;  
Matches 71; Conservative 19; Mismatches 16; Indels 1; Gaps 1;  
QY 1 DIOMTQSPSSLSASVGDRTTCTKTSODINKYMWYOOTPGKAPRLIHYSALQPGIPS 60  
DB 1 DIOMTQSPSSLSASVGDRTTCTKTSODINKYMWYOOTPGKAPRLIHYSALQPGIPS 60  
QY 61 RFGSGSGRDYFTFISSLOPEDIAITYCYLOYDNL-WTFGCGTKVEIK 106  
DB 61 RFGSGSGCTDFTLTISGLLPEDRATYICQOSYTTPTVTFGPGTKVEM 107

RESULT 15  
KVLE\_HUMAN STANDARD; PRT; 108 AA.  
ID AC P01397;  
DC 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 1g kappa chain V-L region DEE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72053133; PubMed=5124396;  
RA Milstein C.P., Deverson E.V.;  
RT "The amino acid sequence of a human kappa light chain.";  
RL Biochem. J. 123:945-958(1971).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR PIR: A01865: KIHUKA.  
DR HSSP: P01607: 1RET.  
DR InterPro: IPR003006: 1g\_MHC.  
DR InterPro: IPR003596: 1g\_V.  
DR Pfam: PF00047: 1g: 1.  
DR SMART: SM00406: IGV: 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT 24 34 FRAMEWORK-1.  
FT 35 49 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT 57 88 FRAMEWORK-3.  
FT 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BDD6350017F1E51 CRC64;

Query Match 69.1%; Score 388.5; DB 1; Length 108;  
Best Local Similarity 68.9%; Pred. No. 3.6e-34;

Matches 73; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
QY 1 DIOMTQSPSSLSASVGDRTTCTKTSODINKYMWYOOTPGKAPRLIHYSALQPGIPS 60  
DB 1 BIZMTQSPSSLSASVGDRTTCTKTSODINKYMWYOOTPGKAPRLIHYSALQPGIPS 60  
QY 61 RFGSGSGRDYFTFISSLOPEDIAITYCYLOYDNL-WTFGCGTKVEIK 106  
DB 61 RFGSGSGCTDFTLTISGLLPEDRATYICQOSYTTPTVTFGPGTKVEM 107

Search completed: July 9, 2002, 15:45:57  
Job time: 373 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:39:09 ; Search time 43.02 Seconds

(Without alignments)  
426.254 Million cell updates/sec

Title: US-09-010-377-1

Sequence: 1 DIOMTOSPSLSASVGDVRYT.....YCLQYDNLWFGQTKVEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: SP\_Archaea:\*
- 2: SP\_Bacteria:\*
- 3: SP\_Fungi:\*
- 4: SP\_Human:\*
- 5: SP\_Invertebrate:\*
- 6: SP\_Mammal:\*
- 7: SP\_Mhc:\*
- 8: SP\_Organelle:\*
- 9: SP\_Phage:\*
- 10: SP\_Plant:\*
- 11: SP\_Proc:\*
- 12: SP\_Virus:\*
- 13: SP\_Vertebrate:\*
- 14: SP\_Unclassified:\*
- 15: SP\_Virus:\*
- 16: SP\_Bacteriophage:\*
- 17: SP\_Archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77	Q9UL77 homo sapien
2	418	74.4	241	11	Q921A6	Q921A6 mus musculu
3	414	73.7	107	4	Q96SA9	Q96SA9 homo sapien
4	406.5	72.3	108	4	Q9UL70	Q9UL70 homo sapien
5	395	70.3	107	4	Q9UL81	Q9UL81 homo sapien
6	385.5	68.6	108	4	Q9UL79	Q9UL79 homo sapien
7	384.5	68.4	214	11	Q91LAS	Q91LAS mus musculu
8	379.5	67.5	233	11	Q91WS9	Q91WS9 mus musculu
9	365.5	65.0	116	4	Q96PF6	Q96PF6 homo sapien
10	362.5	64.5	107	11	Q91L84	Q91L84 mus musculu
11	355.5	63.3	234	11	Q91W88	Q91W88 mus musculu
12	353.5	62.9	109	11	Q920B6	Q920B6 mus musculu
13	337.5	60.1	298	11	Q90YF0	Q90YF0 mus musculu
14	336.5	59.9	108	4	Q9UL83	Q9UL83 homo sapien
15	332	59.1	109	4	Q9UL85	Q9UL85 homo sapien
16	331	58.9	109	4	Q9UL78	Q9UL78 homo sapien

17	329	58.5	109	4	Q9UL86	Q9UL86 homo sapien
18	322.5	57.4	127	11	Q925S9	Q925S9 mus musculu
19	307.5	54.7	107	11	Q9ER29	Q9ER29 mus musculu
20	306.5	54.5	111	11	Q920E9	Q920E9 mus musculu
21	303.5	54.0	211	11	Q91XU0	Q91XU0 mus musculu
22	302.5	53.8	99	11	Q9UL74	Q9UL74 mus musculu
23	297	52.3	106	5	Q9UL40	Q9UL40 mus musculu
24	294	52.8	238	11	Q99M37	Q99M37 mus musculu
25	292.5	52.0	114	4	Q9UL80	Q9UL80 mus musculu
26	284.5	50.6	101	11	Q9UL78	Q9UL78 homo sapien
27	284	50.5	235	11	Q91W12	Q91W12 mus musculu
28	281.5	50.1	97	11	Q9UL76	Q9UL76 mus musculu
29	273.5	48.7	109	6	Q9N0W5	Q9N0W5 oryctolagus
30	269.5	48.0	103	11	Q9JL80	Q9JL80 mus musculu
31	255	45.4	104	11	Q9JL82	Q9JL82 mus musculu
32	212.5	37.8	107	4	Q9UL82	Q9UL82 mus musculu
33	210	37.4	108	4	Q96S80	Q96S80 homo sapien
34	206	36.7	107	4	Q9NSD6	Q9NSD6 homo sapien
35	202	35.9	236	4	Q96E61	Q96E61 homo sapien
36	201	35.8	112	4	Q96JD1	Q96JD1 homo sapien
37	190.5	33.9	112	4	Q96JD2	Q96JD2 homo sapien
38	190.5	33.9	116	4	Q96JDO	Q96JDO homo sapien
39	184	32.7	218	11	Q925S1	Q925S1 mus musculu
40	183	32.6	109	11	Q9ET13	Q9ET13 mus musculu
41	179	31.9	233	11	Q91V32	Q91V32 m adult mal
42	170	30.2	130	4	Q9NP29	Q9NP29 homo sapien
43	168	29.9	235	11	Q99M11	Q99M11 mus musculu
44	166	29.5	233	4	Q96169	Q96169 homo sapien
45	165	29.4	337	13	Q91B02	Q91B02 spherooides

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	108 AA.
Q9UL77	Q9UL77	Q9UL77		
AC	Q9UL77	Q9UL77		
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	*Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.;			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL: AF035037; AAD56273.1; .			
DR	HSSP: P01607; IREI.			
DR	InterPro: IPR003006; Iq_MHC.			
DR	InterPro: IPR003596; Iq_V.			
DR	Pfam: PF00047; Iq_1.			
DR	SMART: SM00406; IqV_1.			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE	108 AA;	11738 MW;	C06681716C4D16F3 CMC64;
Query Match	76.2%;	Score 428.5;	DB 4;	Length 108;
Best Local Similarity	76.6%;	Pred. NO. 1.1e-40;		
Matches	82;	Conservative	8;	Mismatches 16;
				Indels 1;
				Caps 1;
QY	1	DIOMTOSPSLSASVGDVRYTICKTSODINKYMAVYOOTPGKAPRLIHTYSALOPGPS	60	
DB	1	DIOMTOSPSLSASVGDVRYTICKTSODINKYMAVYOOTPGKAPRLIHTYSALOPGPS	60	

QY 61 RFGSGSGRDYFTTISLOPEDATYTCLO-VDNLMTFGGTKVEIK 106  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 61 RFGSGSGRDYFTTISLOPEDATYTCLOVQDSYSTSMTEGEGTKVEIK 107

RESULT 2  
 Q921A6 PRELIMINARY: PRT: 241 AA.

AC Q921A6: 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98170165; PubMed=9509426;  
 RA Chung J.H., Choi S.D., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
 RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
 RT "Cloning and characterization of cDNAs encoding VH and VL of a  
 RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
 RT generation of a single-chain Fv molecule (scfv)."  
 RL Mol. Cells 7:816-819(1997).  
 DR EMBL: U88067; AAB48044.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 241 241  
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 74.4%; Score 418; DB 11; Length 241;  
 Best Local Similarity 73.6%; Pred. No. 4.5e-39;  
 Matches 78; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTYTCCTSDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 134 DIELTQSPSSLSASVGDRTYTCCTSDINKYIAWQHPGKAPRAHLLIHYIQGIPS 193  
 QY 61 RFGSGSGRDYFTTISLOPEDATYTCLOVDNLMTFGGTKVEIK 106  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 194 RFGSGSGRDYFTTISLOPEDATYTCLOVDNLMTFGGTKVEIK 239

RESULT 3  
 Q96SA9 PRELIMINARY: PRT: 107 AA.

AC Q96SA9: 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN  
 DE VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.M.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes."  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL: U96396; AAB68785.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB4359C5B577F16 CRC64;

Query Match 73.7%; Score 414; DB 4; Length 107;  
 Best Local Similarity 75.5%; Pred. No. 4.8e-39;  
 Matches 80; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTYTCCTSDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 1 DIOMTQSPSSLSASVGDRTYTCCTSDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60  
 QY 61 RFGSGSGRDYFTTISLOPEDATYTCLOVDNLMTFGGTKVEIK 106  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 61 RFGSGSGRDYFTTISLOPEDATYTCLOVQDSYSTSMTEGEGTKVEIK 107

RESULT 4  
 Q9UL70 PRELIMINARY: PRT: 108 AA.

AC Q9UL70: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035044; AAD56280.1; -.  
 DR HSSP: P01607; IREI.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 FT NON\_TER 1 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3FA1FCCA37 CRC64;

Query Match 72.3%; Score 406.5; DB 4; Length 108;  
 Best Local Similarity 72.9%; Pred. No. 3.4e-38;  
 Matches 78; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 DIOMTQSPSSLSASVGDRTYTCCTSDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 1 DIOMTQSPSSLSASVGDRTYTCCTSDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60  
 QY 61 RFGSGSGRDYFTTISLOPEDATYTCLOVDNLMTFGGTKVEIK 106  
 ||||| : : : : : ||||| : : : : : ||||| : : : : :  
 Db 61 RFGSGSGRDYFTTISLOPEDATYTCLOVQDSYSTSMTEGEGTKVEIK 107

RESULT 5  
 Q9UL81 PRELIMINARY: PRT: 107 AA.

AC Q9UL81: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RT Young D.C.;  
 RT \*Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.\*;  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035033; AAD56271.1; -.  
 DR HSSP: P01607; IREI.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR InterPro: IPR003596; 1g\_V.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; 1g; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SEQUENCE 107 AA: 11501 MW: 070549FDE0754748 CRC64;

Query Match 70.3%; Score 395; DB 4; Length 107;  
 Best Local Similarity 71.7%; Pred. No. 6.7e-37;  
 Matches 76; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRTVITCKTSODINKYAMVYQOTPGKAPRLIHYTSALQPGIPS 60  
 Db 1 DIOMTQSPSSLSASVGDRTVITCKTSODINKYAMVYQOTPGKAPRLIHYTSALQPGIPS 60  
 OY 61 RFGSGSGRDYFTTSSLOPEDATYTCLODYDNL-WTFGGCTKVEIK 106  
 Db 61 RFGSGSGRDYFTTSSLOPEDATYTCLODYDNL-WTFGGCTKVEIK 106

RESULT 6  
 O9UL79 PRELIMINARY: PRT: 108 AA.  
 ID O9UL79;  
 AC O9UL79;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MOSIN-REACTIVE IMMUNOGLUBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT \*Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.\*;  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035033; AAD56271.1; -.  
 DR HSSP: P01607; IREI.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR InterPro: IPR003596; 1g\_V.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; 1g; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SEQUENCE 108 AA: 11787 MW: DB5845F19724FB4E CRC64;

Query Match 68.6%; Score 385.5; DB 4; Length 108;  
 Best Local Similarity 72.0%; Pred. No. 7.9e-36;  
 Matches 77; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

OY 1 DIOMTQSPSSLSASVGDRTVITCKTSODINKYAMVYQOTPGKAPRLIHYTSALQPGIPS 60  
 Db 1 DIOMTQSPSSLSASVGDRTVITCKTSODINKYAMVYQOTPGKAPRLIHYTSALQPGIPS 60  
 OY 61 RFGSGSGRDYFTTSSLOPEDATYTCLODYDNL-WTFGGCTKVEIK 106  
 Db 61 RFGSGSGRDYFTTSSLOPEDATYTCLODYDNL-WTFGGCTKVEIK 106

RESULT 7  
 O9RIAS PRELIMINARY: PRT: 214 AA.  
 ID O9RIAS;  
 AC O9RIAS;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
 RT \*Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
 RT antibody (Mab 7, its light and heavy chains) and construction of a  
 RT single chain antibody (scFv).  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF152371; AAD40242.1; -.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR003600; 1g\_Like.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR InterPro: IPR003596; 1g\_V.  
 DR Pfam: PF00047; 1g; 2.  
 DR SMART: SM00406; 1g; 1.  
 DR SMART: SM00410; 1g\_Like; 1.  
 DR PROSITE: PS00290; 1g\_MHC; UNKNOWN\_1.  
 FT NON\_TER 1  
 FT NON\_TER 214  
 SEQUENCE 214 AA: 23922 MW: 52BA205FDE95E2A CRC64;

Query Match 68.4%; Score 384.5; DB 11; Length 214;  
 Best Local Similarity 66.4%; Pred. No. 2.3e-35;  
 Matches 71; Conservative 18; Mismatches 17; Indels 1; Gaps 1;

OY 1 DIOMTQSPSSLSASVGDRTVITCKTSODINKYAMVYQOTPGKAPRLIHYTSALQPGIPS 60  
 Db 1 DIOMTQSPSSLSASVGDRTVITCKTSODINKYAMVYQOTPGKAPRLIHYTSALQPGIPS 60  
 OY 61 RFGSGSGRDYFTTSSLOPEDATYTCLODYDNL-WTFGGCTKVEIK 106  
 Db 61 RFGSGSGRDYFTTSSLOPEDATYTCLODYDNL-WTFGGCTKVEIK 106

RESULT 8  
 O9IWS9 PRELIMINARY: PRT: 233 AA.  
 ID O9IWS9;  
 AC O9IWS9;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RA Strussberg R.;  
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC013496; AAH13496.1; -.  
 DR Hypothetical protein.  
 FT NON\_TER 1  
 FT NON\_TER 233  
 SEQUENCE 233 AA: 25781 MW: B1C184DA149A16EB CRC64;

Query Match 67.5%; Score 379.5; DB 11; Length 233;  
 Best Local Similarity 69.2%; Pred. No. 9.2e-35;



RP SEQUENCE FROM N.A.  
RA Alkin J.D., Jape A., Jennings L.G., Horvath O., Cotton R.G.H.,  
RT "Definition of the idiotype of Pterin-Mimicking Antibodies Expressed  
in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF307938; AAL09422.1; -  
FT NON-TER 1 109 109  
FT SEQUENCE 109 AA: 11943 MW: DAD3F98E05DD1501 CRC64;

Query Match 62.9%; Score 353.5; DB 11; Length 109;  
Best Local Similarity 61.7%; Pred. No. 3,2e-32;  
Matches 66; Conservative 16; Mismatches 24; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDVYTTCTKTSODINKYMWYQOTPGKAPRLIHVTSALQGPIS 60  
DB 1 DIOMTOSPSLSASVGEVYTTCTKASGNHNYLAWYQOKCKSPOLLVYNAKTLADGVPS 60  
OY 61 RFGSGSGRDYTTTSSLOPEDATYYCLOY-DNLMTFGCGTKVEIK 106  
DB 61 RFGSGSGCTGYSLKINSLOPEDFGSYCOHFWTPTFGCGTKLEIK 107

RESULT 13  
O90YF0 PRELIMINARY; PRT; 298 AA.

AC O90YF0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CN 8 SCFV.  
GN CN 8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
KC STRAIN-BALB/C; TISSUE-SPLEEN;  
RX MEDLINE=20183931; PubMed=10706631;  
RA Shinozaki N., Demura T., Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
recognizing a cell polarity by using a phage display subtraction  
method."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).  
DR EMBL: AB036341; BAA88633.1; -  
DR HSSP: P01607; JREI.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00406; IgV; 2.  
SO SEQUENCE 298 AA: 31867 MW: E0F96B8A17004317 CRC64;

Query Match 60.1%; Score 337.5; DB 11; Length 298;  
Best Local Similarity 58.9%; Pred. No. 6,6e-30;  
Matches 63; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

OY 1 DIOMTOSPSLSASVGDVYTTCTKTSODINKYMWYQOTPGKAPRLIHVTSALQGPIS 60  
DB 173 DIETOSPASLSASVGEVYTTCTKASGNHNYLAWYQOKCKSPOLLVYNAKTLADGVPS 232  
OY 61 RFGSGSGRDYTTTSSLOPEDATYYCLOY-DNLMTFGCGTKVEIK 106  
DB 233 RFGSGSGCTGYSLKINSLOPEDFGSYCOHFWTPTFGCGTKLEIK 279

RESULT 14  
O90L83 PRELIMINARY; PRT; 108 AA.  
AC O90L83;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Young X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035031; AAD56267.1; -  
DR HSSP: P80362; IWTI.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IgV; 1.  
FT NON-TER 1 108 108  
FT SEQUENCE 108 AA: 11834 MW: 9F9C5A92EBA96EEA CRC64;

Query Match 59.9%; Score 336.5; DB 4; Length 108;  
Best Local Similarity 60.2%; Pred. No. 2,6e-30;  
Matches 65; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

OY 1 DIOMTOSPSLSASVGDVYTTCTKTSODINKYMWYQOTPGKAPRLIHVTSALQGPIS 60  
DB 1 EIYMTSPATLSVSPERATLSCRASQSSNNLAWYQOKRPGQAPRLITCATRATGIPA 60  
OY 61 RFGSGSGRDYTTTSSLOPEDATYYCLOYDNLW--TFGCGTKVEIK 106  
DB 61 RFGSGSGTEFTLTSSLOPEDFAVYCOHNN-WPFTFGPTKVIDK 107

RESULT 15  
O90L85 PRELIMINARY; PRT; 109 AA.  
AC O90L85;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035029; AAD56265.1; -  
DR HSSP: P80362; IWTI.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IgV; 1.  
FT NON-TER 1 109 109  
FT SEQUENCE 109 AA: 11761 MW: FB1E43E7C7AFACCC CRC64;

Query Match 59.1%; Score 332; DB 4; Length 109;



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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:38:34 : Search time 51.18 Seconds

(without alignments)  
230.047 Million cell updates/sec

Title: US-09-010-377-1

Perfect score: 562  
Sequence: 1 DIOMTQSPSSLSASVGDRT.....YCLQYDNLMPFGGKVEIK 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA1981.DAT.\*  
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10: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA1991.DAT.\*  
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19: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/hold-geneeq/geneeq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	106	AA1981321	Humanized anti-VLA
2	562	100.0	106	AAW22412	Humanised alpha-4
3	562	100.0	126	AAW22419	Humanised alpha-4
4	508	90.4	106	AA1981328	Mouse anti-VLA-4 a
5	508	90.4	126	AA1981326	Mouse VLA-4 antibo
6	508	90.4	126	AA1981332	Human VLA-4 reshap
7	508	90.4	126	AAW22409	Alpha-4 integrin m
8	488	86.8	359	AAV29913	Human MCP-3 and mu
9	488	86.8	361	AAV29911	Human IP-10 and mu
10	488	86.8	374	AAV29916	Artificial synthe
11	481	85.6	128	AA1960627	ME1-14 light chain

12	475.5	84.6	234	12	AA13050	CD4-specific CDR-g
13	471.5	83.9	107	16	AA178970	Light chain variab
14	465	82.7	108	17	AA193159	Murine monoclonal
15	460.5	81.9	128	11	AA196252	Variable region of
16	460	81.9	637	13	AA196983	(PRP51)-ETA fusion
17	456	81.1	109	19	AA196797	Anti-gp54 Mab T16
18	455	81.0	240	16	AA196495	SCFV(FW951). Syn
19	455	81.0	241	20	AA191882	Amino acid sequenc
20	455	81.0	245	16	AA196800	Anti-gp54 Mab T16
21	453.5	80.7	107	16	AA196800	Humanized VLA-4 an
22	453.5	80.6	107	18	AA196800	Humanized alpha-4
23	453	80.6	109	12	AA196558	Murine OKT4 light
24	452	80.4	241	13	AA196558	FWP51 fusion prote
25	451.5	80.3	108	16	AA196513	Human RE1 monoclon
26	451.5	80.3	129	15	AA196513	Human/murine IL-1
27	451	80.2	107	19	AA196513	R. pipliens recombi
28	449.5	80.0	107	19	AA196513	Variable light dom
29	449.5	80.0	107	19	AA196513	Humanised murine a
30	446.5	79.4	108	18	AA196513	CDR-grafted light
31	446.5	79.4	110	19	AA196513	Anti-VEGF humanise
32	446.5	79.4	234	18	AA196513	TF8-509 CDR-graft
33	446.5	79.4	237	19	AA196513	Protein encoded by
34	445.5	79.3	107	19	AA196513	Variable light dom
35	445.5	79.3	107	19	AA196513	Humanised murine a
36	444.5	79.1	107	20	AA196513	Humanised anti-4p
37	444.5	79.1	107	22	AA196513	Human VI consensus
38	444.5	79.1	107	22	AA196513	Consensus human 11
39	444.5	79.1	107	22	AA196513	Human variable 119
40	444.5	79.1	108	19	AA196513	Human consensus fr
41	444.5	79.1	108	21	AA196513	Human consensus se
42	444.5	79.1	126	13	AA196513	pUC-RV1-PM1a. Syn
43	444.5	79.1	126	13	AA196513	pUC-RV1-PM1a. Syn
44	444.5	79.1	256	21	AA196513	Interleukin-6 spec
45	444.5	79.1	260	21	AA196513	Single chain fv pr

#### ALIGNMENTS

RESULT 1	AA1981321	standard; Protein: 106 AA.
XX	AA1981321:	
AC	02-APR-1996 (first entry)	
DT	Humanized anti-VLA-4 antibody 21.6 light chain variable region, Ia.	
XX	Humanized antibody: leukocyte adhesion molecule; VLA-4; therapeutic;	
XX	antibody engineering.	
KW	Chimeric Mus musculus.	
XX	OS Chimeric Homo sapiens.	
OS	W09519790-A1.	
XX	27-JUL-1995.	
PD	25-JAN-1995: 95MO-DS01219.	
XX	25-JAN-1995: 94US-0186269.	
PR	(ATHE-) ATHENA NEUROSCIENCES INC.	
PA	Bending MM, Jones TS, Leger OJ, Saldanha J:	
XX	WPI: 1995-269276/35.	
DR	New humanised antibodies against VLA-4 - used for inhibiting	
PT	leukocyte adhesion to endothelial cells, partic. for treating	
PT	inflammatory disease.	
XX		

PS Claim 9, Page 67; 105pp; English.

XX The sequence encodes the humanized mouse antibody 21.6 light chain

CC variable region, Ia, directed against leukocyte adhesion molecule

CC VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AA09889 and

CC AA09892) regions are linked to human constant regions in the

CC construction of a humanized antibody against VLA-4. The 5' and 3'

CC ends of the mouse cDNAs are modified using PCR primers (See

CC AA09895-98) and then subcloned into mammalian cell expression vectors

CC containing human kappa or gamma-1 constant regions. In the humanized

CC light chain, amino acids L45, L49, L58 and L69 in the human kappa LC

CC VR framework are replaced by the amino acid present in the equivalent

CC position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric

CC antibodies are transfected into COS cells. The humanized antibodies

CC can be used for inhibiting adhesion of a leukocyte to an endothelial

CC cell and for treating inflammatory diseases such as multiple

CC sclerosis. They can also be used in the treatment of stroke,

CC cerebral trauma, meningitis or encephalitis. The antibodies can

CC also be used for detecting VLA-4, for affinity purification or for

CC generating anti-idiotypic antibodies.

XX

SQ Sequence 106 AA:

Query Match 100.0%; Score 562; DB 16; Length 106;

Best Local Similarity 100.0%; Pred. No. 1e-36;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIOMTOSPSLSASVGDRTTICKTSODINKYMAWYOOTPGKAPRLTHYSALQGPIS 60

DB 1 dltmqgspsslsasvgydvrttcktsqgdnkymayqgqpykaptllyhsalqgpls 60

OY 61 RFGSGSGGRDYTTTSLQPEDIAITYCLOYDNLTWTFGQGRKVEIK 106

DB 61 rfsqsgsgdyfttsslqpediatytcloydnltwtfqgrkveik 106

RESULT 2

AAW22412

ID AAW22412 standard; Protein; 106 AA.

AC AAW22412;

XX

DT 08-DEC-1997 (first entry)

XX

DE Humanised alpha-4 integrin antibody 21.6 VL Ia.

XX

KW Alpha-4 integrin: humanised antibody; monoclonal antibody 21.6;

KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;

KW metastasis; inflammatory bowel disease; rheumatoid arthritis;

KW transplant rejection; graft versus host disease; nephritis;

KW atopic dermatitis; psoriasis; myocardial ischemia;

KW acute leukocyte mediated lung injury; therapy.

XX

OS Chimeric Mus musculus;

OS Chimeric Homo sapiens;

OS Chimeric synthetic.

XX

Key location/Qualifiers

FT Region 1..23

FT /label= FR1

FT /note= "REI framework region 1"

FT Region 24..34

FT /label= CDR1

FT /note= "21.6 complementarity determining region 1"

FT Region 35..49

FT /label= FR2

FT /note= "REI framework region 2"

FT Misc-difference 45

FT /note= "REI Lys-45 is substd. by Lys of mouse

FT 21.6 VL, important in supporting the

FT Misc-difference 49

FT CDR2 loop"

FT /note= "REI Tyr-49 is substd. by His of mouse

FT 21.6 VL, located at the binding site"

FT Region 50..56

FT /label= CDR2

FT /note= "21.6 complementarity determining region 2"

FT Region 57..88

FT /label= FR3

FT /note= "REI framework region 3"

FT Misc-difference 58

FT /note= "REI Val-58 is substd. by Ile of mouse

FT 21.6 VL, important in supporting the CDR2

FT loop"

FT Misc-difference 69

FT /note= "REI Thr-69 is substd. by Arg of mouse

FT 21.6 VL, involved in antibody-antigen

FT binding"

FT Region 89..96

FT /label= CDR3

FT /note= "21.6 complementarity determining region 3"

FT Region 97..106

FT /label= FR4

FT /note= "REI framework region 4"

FT Misc-difference 103

FT /note= "REI Leu-103 substd. by Val, more typical

FT of human kappa light chain J region"

FT Misc-difference 104

FT /note= "REI Gln-104 substd. by Glu, more typical

FT of human kappa light chain J region"

FT Misc-difference 106

FT /note= "REI Thr-106 substd. by Lys, more typical

FT of human kappa light chain J region"

XX WO9718838-A1.

XX

PD 29-MAY-1997.

XX

PE 21-NOV-1996; 96WO-US18807.

XX

PR 21-NOV-1995; 95US-0561521.

XX

PA (ATHE-) ATHENA NEUROSCIENCES INC.

XX

PI Bending MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;

XX

DR WPI; 1997-297879/27.

XX

PT Uses of humanised alpha-4 integrin antibody - for treatment of

PT asthma, atherosclerosis, AIDS, dementia, etc.

XX

PS Claim 25; Fig 6; 107pp; English.

XX

CC This polypeptide, designated Ia, comprises the light chain variable

CC region (VL) of a humanised alpha-4 integrin antibody 21.6. It is

CC composed of complementarity determining regions (CDRs) from the VL

CC region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody

CC 21.6 and a modified human REI framework. It can be expressed in

CC mammalian host cells following PCR amplification and mutagenesis

CC of appropriate fragments of mouse and human DNA sequences. The

CC humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used

CC to produce a claimed humanised 21.6 antibody that is useful in the

CC manufacture of a medicament for treating asthma, atherosclerosis,

CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid

CC arthritis, transplant rejection, graft versus host disease, tumour

CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial

CC ischemia, and acute leukocyte mediated lung injury. The antibody

CC may also be used in the affinity purification of alpha-4 integrin

CC for use as a vaccine or an immunogen. It is also useful for

CC generating idiotypic antibodies. The humanised antibody has a

CC half-life in the human circulation essentially equivalent to that

CC of naturally occurring human antibodies.

XX

SQ Sequence 106 AA:

Query Match 100.0%; Score 562; DB 18; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1e-36;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIQMTGSPSSISASVGRVTITCTKTSODINKYMAWYOOTPGKAPRLIHTSALPGIPS 60  
 Db 1 diqmtgspssisasvgrvtitctktsodinkymawyqpgkaprllihysalpgips 60  
 OY 61 RFGSGSGRDYFTTISLQPEDIAITYYCLQYDNLMTFGGCTKVEIK 106  
 Db 61 rfgsgsgrdyfttislqpediatyyclyqydnltwfggctkveik 106

## RESULT 3

AAW22419 standard; Protein; 126 AA.

AAW22419;

08-DEC-1997 (first entry)

Humanised alpha-4 integrin antibody 21.6 VL version La.

Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
 asthina; atherosclerosis; AIDS; dementia; diabetes; tumour;  
 metastasis; inflammatory bowel disease; rheumatoid arthritis;  
 transplant rejection; graft versus host disease; nephritis;  
 atopic dermatitis; psoriasis; myocardial ischaemia;  
 acute leukocyte mediated lung injury; therapy.

Chimeric Mus musculus;  
 Chimeric Homo sapiens;  
 Chimeric synthetic.

Key Location/Qualifiers  
 Reptide 1..20  
 Protein 21..126  
 /label= Mat.protein  
 /note= "VL version La (Claim 25)"  
 Region 21..43  
 /label= FR1  
 /note= "RE1 framework region 1"  
 Region 44..54  
 /label= CDR1  
 /note= "21.6 complementarity determining region 1"  
 Region 55..69  
 /label= FR2  
 /note= "RE1 framework region 2"  
 Region 70..76  
 /label= CDR2  
 /note= "21.6 complementarity determining region 2"  
 Region 77..108  
 /label= FR3  
 /note= "RE1 framework region 3"  
 Region 109..116  
 /label= CDR3  
 /note= "21.6 complementarity determining region 3"  
 Region 117..126  
 /label= FR4  
 /note= "RE1 framework region 4"

MO9718838-A1.  
 29-MAY-1997.  
 21-NOV-1996; 96WO-US18807.  
 21-NOV-1995; 95US-0561521.  
 (ATHE-) ATHENA NEUROSCIENCES INC.

PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;  
 DR WPI: 1997-297879/27.  
 DR N-PSDB; AAT74788.

Uses of humanised alpha-4 integrin antibody - for treatment of  
 PT asthma, atherosclerosis, AIDS, dementia, etc.

PS Example 6; Fig 10; 107pp; English.

CC This polypeptide, designated Ia, comprises the light chain variable  
 CC region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also  
 CC AAW22412). It is composed of complementarity determining regions from  
 CC the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal  
 CC antibody 21.6 and a modified human RE1 framework. It can be  
 CC expressed in mammalian host cells following PCR amplification and  
 CC mutagenesis of appropriate mouse and human DNA sequences. The  
 CC humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used  
 CC to produce a claimed humanised 21.6 antibody that is useful in the  
 CC manufacture of a medicament for treating asthma, atherosclerosis,  
 CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid  
 CC arthritis, transplant rejection, graft versus host disease, tumour  
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial  
 CC ischaemia, and acute leukocyte mediated lung injury. The humanised  
 CC antibody has a half-life in the human circulation essentially  
 CC equivalent to that of naturally occurring human antibodies.

Sequence 126 AA:

Query Match 100.0%; Score 562; DB 18; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-36;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIQMTGSPSSISASVGRVTITCTKTSODINKYMAWYOOTPGKAPRLIHTSALPGIPS 60  
 Db 21 diqmtgspssisasvgrvtitctktsodinkymawyqpgkaprllihysalpgips 80  
 OY 61 RFGSGSGRDYFTTISLQPEDIAITYYCLQYDNLMTFGGCTKVEIK 106  
 Db 81 rfgsgsgrdyfttislqpediatyyclyqydnltwfggctkveik 126

## RESULT 4

AAW22419 standard; Protein; 106 AA.

AAW22419;

02-APR-1996 (first entry)

Mouse anti-VLA-4 antibody 21.6 light chain variable region.

Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
 antibody engineering.

Mus musculus.

Key Location/Qualifiers  
 Region 1..23  
 /label= FR1  
 /note= "mouse light chain variable framework  
 region 1"

Region 24..34

Region 35..49  
 /label= FR2  
 /note= "mouse light chain variable complementarity  
 determining region 1"

Region 50..56

Region 57..67  
 /label= CDR2

FT /note= "mouse light chain variable complementarity  
 FT determining region 2"  
 FT Region  
 FT 57..88  
 FT /label= FR3  
 FT /note= "mouse light chain variable framework  
 FT region 3"  
 FT Region  
 FT 89..96  
 FT /label= CDR3  
 FT /note= "mouse light chain variable complementarity  
 FT determining region 3"  
 FT Region  
 FT 97..106  
 FT /label= FR4  
 FT /note= "mouse light chain variable framework  
 FT region 4"  
 FT W09519790-A1.  
 PD 27-JUL-1995.  
 XX 25-JAN-1995; 95WO-US01219.  
 XX 25-JAN-1994; 94US-0186269.  
 XX (ATHE-) ATHENA NEUROSCIENCES INC.  
 XX Bendig MM, Jones TS, Leger OJ, Saldanha J;  
 XX WPI: 1995-269276/35.  
 XX New humanised antibodies against VLA-4 - used for inhibiting  
 PT leukocyte adhesion to endothelial cells, partic. for treating  
 PT inflammatory disease.  
 XX Disclosure: Page 66; 105pp; English.

CC The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain  
 CC variable region (without signal sequence). Cloned cDNA CDR sequences of  
 CC mouse 21.6 variable light and variable heavy regions are linked to human  
 CC constant framework regions of the REI antibody for the light chain and  
 CC the 2\*CI antibody for the heavy chain in the construction of a humanized  
 CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are  
 CC modified using PCR primers (See AAQ99895-98) and then subcloned into  
 CC mammalian cell expression vectors containing human kappa or gamma-1  
 CC constant regions. In the humanized light chain, amino acids L45, L49,  
 CC L58 and L69 in the human kappa LCVR framework are replaced by the amino  
 CC acid present in the equivalent position of the mouse 21.6 Ig light  
 CC chain. Plasmids encoding the chimeric antibodies are transfected into COS  
 CC cells. The humanized antibodies can be used to inhibit adhesion of a  
 CC leukocyte to an endothelial cell and to treat inflammatory diseases such  
 CC as multiple sclerosis. They can also be used in the treatment of stroke,  
 CC cerebral traumas, meningitis or encephalitis. The antibodies can also be  
 CC used for detecting VLA-4, for affinity purification or for generating  
 CC anti-idiotypic antibodies.

XX Sequence 106 AA:

Query Match 90.4%; Score 508; DB 16; length 106;  
 Best local similarity 88.7%; Pred. No. 1.5e-32;  
 Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIOMTOSPSLSASVGDRTYITCKTSQDINKYMWYQQTGKAPRLIHTSLQGPIS 60  
 DB 1 dimgtqspsslsaslgkvtlctsqdinkymawybqbpqyrprllihytalslqgips 60  
 QY 61 RFGSGSGRDYFTTISLQPEQATYYCQYONLMTFEGGTKEIK 106  
 DB 61 rtsgsgsgrdyfttisslqpeqatyycaydnltwtfgggtkietk 106

RESULT 5  
 AAR81326  
 ID AAR81326 standard; Protein: 126 AA.

XX AAR81326;  
 AC 23-MAR-1996 (first entry)  
 DT Mouse VLA-4 antibody 21.6 light chain variable region.  
 XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
 KW antibody engineering.  
 XX Mus musculus.  
 OS  
 FH Key  
 FT Peptide  
 FT 1..20  
 FT /note= "signal peptide"  
 FT Region  
 FT 21..43  
 FT /note= "framework region 1"  
 FT Region  
 FT 44..54  
 FT /note= "complementarity determining region 1"  
 FT Region  
 FT 55..69  
 FT /note= "framework region 2"  
 FT Region  
 FT 70..76  
 FT /note= "complementarity determining region 2"  
 FT Region  
 FT 77..108  
 FT /note= "framework region 3"  
 FT Region  
 FT 109..116  
 FT /note= "complementarity determining region 3"  
 FT Region  
 FT 117..126  
 FT /note= "framework region 4"

XX W09519790-A1.  
 XX 27-JUL-1995.  
 XX 25-JAN-1995; 95WO-US01219.  
 XX 25-JAN-1994; 94US-0186269.  
 XX (ATHE-) ATHENA NEUROSCIENCES INC.  
 XX Bendig MM, Jones TS, Leger OJ, Saldanha J;  
 XX WPI: 1995-269276/35.  
 XX N-PSDB: AAQ99889.

PT New humanised antibodies against VLA-4 - used for inhibiting  
 PT leukocyte adhesion to endothelial cells, partic. for treating  
 PT inflammatory disease.

PS Disclosure: Fig 1; 105pp; English.

CC The sequence represents the mouse antibody 21.6 light chain variable  
 CC region directed against leukocyte adhesion molecule VLA-4. Cloned  
 CC cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are  
 CC linked to human constant regions in the construction of a humanized  
 CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are  
 CC modified using PCR primers (See AAQ99895-98) and then subcloned into  
 CC mammalian cell expression vectors containing human kappa or gamma-1  
 CC constant regions. In the humanized light chain, amino acids L45,  
 CC L49, L58 and L69 in the human kappa LC VR framework are replaced  
 CC by the amino acid present in the equivalent position of the mouse  
 CC 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are  
 CC transfected into COS cells. The humanized antibodies can be used  
 CC to inhibit adhesion of a leukocyte to an endothelial cell and  
 CC to treat inflammatory diseases such as multiple sclerosis. They  
 CC can also be used in the treatment of stroke, cerebral traumas,  
 CC meningitis or encephalitis. The antibodies can also be used for  
 CC detecting VLA-4, for affinity purification or for generating  
 CC anti-idiotypic antibodies.

SO Sequence 126 AA:



Query Match	90.4%	Score 508	DB 16	Length 126
Best Local Similarity	88.7%	Pred. No. 1,8e-32		
Matches 94	Conservative	6	Mismatches 6	Indels 0
				Gaps
OY	1 DIOMOSPSISASVGDVVTITCTKSODIKRYAMVQOTPGKAPRLIHVTSALQCPIS 60			
Db	21 dlmblspsslsaslygkvrltclctsgdlnkymawqnhkprkrlilhysalqpsps 80			
OY	61 RFGSGSGRDYFTTISLQPEDIAATVYICLOYDNLMTFGCGTVEIK 106			
Db	81 rfsgsgsgrdysfnslnlepedlatcyqlghnlwtfggkrltclk 126			
RESULT 6				
ID	AAH81332 standard; Protein: 126 AA.			
XX	AAH81332:			
AC	AAH81332:			
XX	23-MAR-1996 (first entry)			
XX				
DT				
XX	Human VLA-4 reshaped antibody 21.6 light chain variable region.			
DE				
XX				
XX	Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;			
KM	antibody engineering.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Peptide	1..20		
FT		/note="signal peptide"		
FT		21..43		
FT	Region	/note="framework region 1"		
FT		44..54		
FT	Region	/note="complementarity determining region 1"		
FT		55..69		
FT	Region	/note="framework region 2"		
FT		70..76		
FT	Region	/note="complementarity determining region 2"		
FT		77..108		
FT	Region	/note="framework region 3"		
FT		109..116		
FT	Region	/note="complementarity determining region 3"		
FT		117..126		
FT	Region	/note="framework region 4"		
XX				
PN	MO9519790-A1.			
XX				
PD	27-JUL-1995.			
XX				
XX	25-JAN-1995:	95WO-US01219.		
PF				
XX	25-JAN-1994:	94US-0186269.		
PR				
XX	(ATHE-) ATHENA NEUROSCIENCES INC.			
XX				
PA				
XX	Bendig MM, Jones TS, Leger OJ, Saldanha J;			
PI				
XX	WPI; 1995-269276/35.			
DR				
DR	N-PSDB; AA099893.			
PT				
PT	New humanised antibodies against VLA-4 - used for inhibiting			
PT	leukocyte adhesion to endothelial cells, partic. for treating			
PT	inflammatory disease.			
XX				
PS	Disclosure: Fig 10; 105pp; English.			
XX				
CC	The sequence represents the human reshaped antibody 21.6 light			
CC	chain variable region against leukocyte adhesion molecule VLA-4.			
CC	Closed cDNA sequences of mouse 21.6 VL (AA099889) and VH (AA099892			
CC	regions are linked to human constant regions in the construction			
CC	of a humanized antibody against VLA-4. The 5' and 3' ends of the			
CC	mouse cDNAs are modified using PCR primers (See AA099895-98) and			

CC then subcloned into mammalian cell expression vectors containing  
CC human kappa or gamma-1 constant regions. In the humanized light  
CC chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR  
CC framework are replaced by the amino acid present in the equivalent  
CC position of the mouse 21.6 Ig L chain. Plasmids encoding the  
CC chimeric antibodies are transfected into COS cells. The humanized  
CC antibodies can be used to inhibit adhesion of a leukocyte to an  
CC endothelial cell and to treat inflammatory diseases such as  
CC multiple sclerosis. They can also be used in the treatment of  
CC stroke, cerebral trauma, meningitis or encephalitis. The  
CC antibodies can also be used for detecting VLA-4, for affinity  
CC purification or for generating anti-idiotypic antibodies.

Query Match	90.4%	Score 508;	DB 16;	Length 126;
Best Local Similarity	88.7%	Pred. No. 1,8e-32;		
Matches	94; Conservative	6; Mismatches	6; Indels	0; Caps
QY	1 DIQMTRSSSLASVGRDVTICTKTSODINKMAMVOOTPGKAPRLIHNTSALQPIPS	60		
Dd	21 dIQmTqpsSIssAsgkvltctcsgdlnkymawvqhnpqrprlllhysalqpips	80		
QY	61 RFGSGSGRDYFTFISSLQPEDIATYYCLOYDLMTFEGGCTVEIK	106		
Dd	81 rfgsgsgrdygfinslmepediatyyclgdnlwtifgggtlk	126		

AAW22409	7
ID	AAW22409 standard; Protein; 126 AA.
XX	
AC	AAW22409;
XX	
DT	08-DEC-1997 (first entry)
XX	
DE	Alpha-4 integrin mouse MAb 2I.6 VL region.
XX	
XX	Alpha-4 integrin; humanised antibody; monoclonal antibody 2I.6
KW	asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW	metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW	transplant rejection; graft versus host disease; nephritis;
KW	atopic dermatitis; psoriasis; myocardial ischaemia;
KW	acute leukocyte mediated lung injury; therapy.
OS	Mus musculus.
XX	

XX	Key	location/Qualifiers
FT	Peptide	1..20
FT		/label= leader
FT	Region	21..43
FT		/label= FR1
FT		/note= "framework region 1"
FT	Region	44..54
FT		/label= CDR1
FT		/note= "complementarity determining region 1"
FT	Region	55..69
FT		/label= FR2
FT		/note= "framework region 2"
FT	Region	70..76
FT		/label= CDR2
FT		/note= "complementarity determining region 2"
FT	Region	77..108
FT		/label= FR3
FT		/note= "framework region 3"
FT	Region	109..116
FT		/label= CDR3
FT		/note= "complementarity determining region 3"
FT	Region	117..126
FT		/label= FR4
FT		/note= "framework region 4"
XX		

PN WO9718838-A1.  
 XX  
 PD 29-MAY-1997.  
 XX  
 XX  
 PF 21-NOV-1996: 96WO-US18807.  
 XX  
 PR 21-NOV-1995: 95US-0561521.  
 XX  
 PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 XX  
 PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;  
 XX  
 DR WPI: 1997-297879/27.  
 DR N-PSDB: AAT74759.  
 XX  
 PT Uses of humanised alpha-4 integrin antibody - for treatment of  
 PT asthma, atherosclerosis, AIDS, dementia, etc.  
 XX  
 PS Claim 18: Page 68; 107pp; English.  
 XX  
 CC This polypeptide comprises the light chain variable region (VL) of  
 CC mouse anti-alpha-4 integrin monoclonal antibody 21.6. The  
 CC complementarity determining regions (CDRs) of the 21.6 VL can be  
 CC incorporated into a human REI framework to produce a claimed  
 CC humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6  
 CC antibody that is used in the manufacture of a medicament for  
 CC treating a disease selected from asthma, atherosclerosis, AIDS,  
 CC arthritis, transplant rejection, graft versus host disease, tumour  
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial  
 CC ischaemia, and acute leukocyte mediated lung injury. The antibody  
 CC may also be used in the affinity purification of alpha-4 integrin  
 CC for use as a vaccine or an immunogen. It is also useful for  
 CC generating idiotypic antibodies. The humanised antibodies of the  
 CC invention have a half-life in the human circulation essentially  
 CC equivalent to that of naturally occurring human antibodies.  
 XX  
 SQ Sequence 126 AA:  
 Query Match 90.4%; Score 508; DB 18; Length 126;  
 Best Local Similarity 88.7%; Pred. No. 1.8e-32;  
 Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIQMTSPSSLSASVGDRTVTCTKTSODINKYMAWYQOTPGKAPRLIHYTSALQPGIPS 60  
 DB 21 dqlmtspsslsaslgkvltlcktsqdkinkymawyqkpkprllihytsalqpgips 80  
 QY 61 RFGSGSGGRDYFTTSSLOPEDIAITYCYLOYDNLMTREGGKVEIK 106  
 DB 81 rfgsgsggrdyfsslnlepediatyacydnlmtf9ggtkleik 126  
 RESULT 8  
 AAY29913  
 ID AAY29913 standard; Protein: 359 AA.  
 AC AAY29913;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Human MCP-3 and murine scfv38 fusion protein.  
 XX  
 KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
 KW immune response; HIV; infection.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO9946392-A1.  
 XX  
 PD 16-SEP-1999.

XX  
 PF 12-MAR-1999: 99WO-US05345.  
 XX  
 XX 12-MAR-1998: 98US-0077745.  
 XX  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Kwak LW, Biragyn A;  
 XX  
 DR WPI: 1999-551418/46.  
 XX  
 PT New fusion polypeptides comprising a chemokine and a tumour antigen or  
 PT HIV antigen, used for treating cancers or treating or preventing HIV  
 PT infection  
 XX  
 PS Disclosure: Page 118-119; 142pp; English.  
 XX  
 CC The present invention describes fusion proteins comprising a chemokine  
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins  
 CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human  
 CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;  
 CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human  
 CC HIV gp120; (5) human IP-10 and HIV gp120; (6) human MCP-3 and  
 CC gp120. The fusion proteins, and nucleotide sequences encoding them, can  
 CC be used for producing an immune response, e.g. an effector T cell immune  
 CC response. They can also be used for treating cancer or treating or  
 CC preventing HIV infection. The fusion proteins and/or nucleotide sequences  
 CC can be used in in vitro diagnostic assays, as well as in screening assays  
 CC for identifying unknown tumour antigen epitopes and fine mapping of  
 CC tumour antigen epitopes. The present sequence represents a fusion protein  
 CC from the present invention.  
 XX  
 SQ Sequence 359 AA:  
 Query Match 86.8%; Score 488; DB 20; Length 359;  
 Best Local Similarity 84.9%; Pred. No. 1.7e-30;  
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 DIQMTSPSSLSASVGDRTVTCTKTSODINKYMAWYQOTPGKAPRLIHYTSALQPGIPS 60  
 DB 233 dqlmtspsslsaslgkvltlcktsqdkinkymawyqkpkprllihytsalqpgips 292  
 QY 61 RFGSGSGGRDYFTTSSLOPEDIAITYCYLOYDNLMTREGGKVEIK 106  
 DB 293 rfgsgsggrdyfsslnlepediatyacydnlmtf9ggtkleik 338  
 RESULT 9  
 AAY29911  
 ID AAY29911 standard; Protein: 361 AA.  
 AC AAY29911;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Human IP-10 and murine scfv38 fusion protein.  
 XX  
 KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
 KW immune response; HIV; infection.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO9946392-A1.  
 XX  
 PD 16-SEP-1999.  
 PF 12-MAR-1999: 99WO-US05345.  
 XX  
 PR 12-MAR-1998: 98US-0077745.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Kwak LM, Biragyn A;  
 PI WPI: 1999-551418/46.  
 DR  
 XX  
 PT New fusion polypeptides comprising a chemokine and a tumour antigen or  
 PT HIV antigen, used for treating cancers or treating or preventing HIV  
 PT infection.  
 PS Disclosure: Page 115-116; 142pp; English.  
 XX  
 CC The present invention describes fusion proteins comprising a chemokine  
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins  
 CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human  
 CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human  
 CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (4) human  
 CC HIV gp120; (7) human MDC and HIV gp120; (6) human MCP-3 and  
 CC gp120. The fusion proteins, and nucleotide sequences encoding them, can  
 CC be used for producing an immune response, e.g. an effector T cell immune  
 CC response. They can also be used for treating cancer or treating or  
 CC preventing HIV infection. The fusion proteins and/or nucleotide sequences  
 CC can be used in in vitro diagnostic assays, as well as in screening assays  
 CC for identifying unknown tumour antigen epitopes and fine mapping of  
 CC tumour antigen epitopes. The present sequence represents a fusion protein  
 CC from the present invention.  
 XX  
 SO Sequence 361 AA:  
 Query Match 86.8%; Score 488; DB 20; Length 361;  
 Best Local Similarity 84.9%; Pred. No. 1.7e-30;  
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
 Oy 1 DIOMTQSPSSASVGDRTTCTKTSODINKYMWYOOTPGKAPRLIHYTSALOPGIPS 60  
 Db 235 dltmqspsslsaslgvltlckasqdknylawyqkpkpgkprlllhytscltpgips 294  
 Oy 61 RFSGSGSGRDYFTTSSLOPEDIAITYCYLOYNLMTFGCGTRVEIK 106  
 Db 295 rfsqsgsgrdyftsslslopediatyacylgydnlytfgggtkltk 340  
 RESULT 10  
 AAY29916  
 ID AAY29916 standard; Protein: 374 AA.  
 XX  
 AC AAY29916;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Artificial synthetic construct protein SEQ ID NO:15.  
 XX  
 KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;  
 KW Immune response; HIV; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO946392-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 12-MAR-1999; 99MO-US05345.  
 XX  
 PR 12-MAR-1999; 98US-0077745.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Kwak LM, Biragyn A;  
 PI WPI: 1999-551418/46.  
 DR

XX New fusion polypeptides comprising a chemokine and a tumour antigen or  
 PT HIV antigen, used for treating cancers or treating or preventing HIV  
 PT infection.  
 PS Disclosure: Page 117-118; 142pp; English.  
 XX  
 CC The present invention describes fusion proteins comprising a chemokine  
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion  
 CC proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and  
 CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human  
 CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)  
 CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; (6) human  
 CC MCP-3 and HIV gp120; (5) human IP-10 and HIV gp120; and (8) human SDF-1 and  
 CC can be used for producing an immune response, e.g. an effector T cell  
 CC immune response. They can also be used for treating cancer or treating  
 CC or preventing HIV infection. The fusion proteins and/or nucleotide  
 CC sequences can be used in in vitro diagnostic assays, as well as in  
 CC screening assays for identifying unknown tumour antigen epitopes and fine  
 CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are  
 CC are not mentioned further within the specification.  
 XX  
 SO Sequence 374 AA:  
 Query Match 86.8%; Score 488; DB 20; Length 374;  
 Best Local Similarity 84.9%; Pred. No. 1.7e-30;  
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
 Oy 1 DIOMTQSPSSASVGDRTTCTKTSODINKYMWYOOTPGKAPRLIHYTSALOPGIPS 60  
 Db 95 dltmqspsslsaslgvltlckasqdknylawyqkpkpgkprlllhytscltpgips 154  
 Oy 61 RFSGSGSGRDYFTTSSLOPEDIAITYCYLOYNLMTFGCGTRVEIK 106  
 Db 155 rfsqsgsgrdyftsslslopediatyacylgydnlytfgggtkltk 200  
 RESULT 11  
 AAR60627  
 ID AAR60627 standard; Protein: 128 AA.  
 XX  
 AC AAR60627;  
 XX  
 DT 04-JUN-1995 (first entry)  
 XX  
 DE MEL-14 light chain variable region.  
 XX  
 KW Monoclonal antibody; tumour.  
 KW Homo sapiens.  
 OS  
 PN WO9421294-A.  
 XX  
 PD 29-SEP-1994.  
 XX  
 PF 14-MAR-1994; 94MO-US02724.  
 XX  
 PR 19-MAR-1993; 93US-0033864.  
 XX  
 PA (BIGNER) BIGNER D D.  
 PA (CARR/) CARREL S.  
 PA (ZALU/) ZALUTSKY M R.  
 XX  
 PI Bigner DD, Carrel S, Zalutsky MR.  
 XX  
 DR WPI: 1994-316669/39.  
 DR N-PSDB: AAQ73537.  
 XX  
 PT Method of treating solid or cystic tumours with antibodies - by  
 PT administering monoclonal antibody Mel-14, having Fc deleted,

PT using injection or deposition in the cyst cavity

XX PS Disclosure; Fig 2, 31pp; English.

XX CC The sequence is that of the ME1-14 light chain. The protein is a

CC monoclonal antibody which can be administered to treat solid or

CC cystic tumours.

CC See also AAR60626.

XX SQ Sequence 128 AA;

Query Match 85.6%; Score 481; DB 15; Length 128;

Best Local Similarity 84.0%; Pred. No. 2.3e-30;

Matches 89; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITITCKTSQDINKYAWYQQTGPKAPRLIHYTSALQPGIPS 60

DB 21 diqmtqspsslsasvgrvlttcktsqsdinkylawyqpkpkrllmhytsalqpgips 80

QY 61 RFSGSGSGRDYFTTISLQPEDATATYCYDNLMTFGGTKEIK 106

DB 81 rfsqsgsgrdyfttisslqpediatyccydnllmtfggtkeik 126

RESULT 12

AAAR13050 standard; Protein: 234 AA.

XX AC AAR13050;

XX DT 27-SEP-1991 (first entry)

XX DE CD4-specific CDR-grafted light chain.

XX DE variable region; antibody; OKT4A; heavy chain; CD4;

XX KM complementarity determining region.

XX OS Synthetic.

XX FH Key

XX FT Location/Qualifiers

FT 1..20 /label= signal sequence

FT 21..45 /label= framework region 1

FT 46..52 /label= CDR 1

FT 53..69 /label= framework region 2

FT 70..76 /label= CDR 2

FT 77..110 /label= framework region 3

FT 111..116 /label= CDR 3

FT 117..132 /label= framework region 4

FT 133..234 /label= kappa constant domain

XX PN WO9109966-A.

XX PD 11-JUL-1991.

XX PF 21-DEC-1990; 90WO-GB02015.

XX PR 21-DEC-1989; 89GB-0028874.

XX PR 21-DEC-1990; 90WO-GB02017.

XX PR 21-DEC-1990; 90WO-GB02018.

XX PA (ORTH ) ORTHO PHARM CORP.

XX PI Jolliffe LK, Zivian RA, Pulito VL, Adair JR, Athwal DS;

XX DR WPI; 1991-222914/30.

XX DR N-PSDB; AAQ12633.

XX PT New CD4 specific recombinant - complementarity determining region

PT grafted antibody for treating graft rejection and T cell

PT disorders

XX PS Claim 1; Fig 8; 96pp; English.

XX CC This is an example of a CDR-grafted light chain of the invention.

CC The constant regions are based on sequences of the human kappa

CC constant domain, the signal sequence is derived from murine Mab

CC 872.3 and the CDR sequences are based on the murine OKT4A light chain

CC CDRs. The recombinant antibody encoded by this sequence has affinity

CC for CD4 similar to that of OKT4A.

CC See also AAQ12627-012632.

XX SQ Sequence 234 AA;

Query Match 84.6%; Score 475.5; DB 12; Length 234;

Best Local Similarity 84.9%; Pred. No. 1e-29;

Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITITCKTSQDINKYAWYQQTGPKAPRLIHYTSALQPGIPS 60

DB 21 diqmtqspsslsasvgrvlttcktsqsdinkylawyqpkpkrllmhytsalqpgyps 80

QY 61 RFSGSGSGRDYFTTISLQPEDATATYCYDNLMTFGGTKEIK 105

DB 81 rfsqsgsgrdyfttisslqpediatyccydnllmtfggtkeik 126

RESULT 13

AAAR78970 standard; Protein: 107 AA.

XX AC AAR78970;

XX DT 21-DEC-1995 (first entry)

XX DE Light chain variable region for monoclonal antibody 23F8.

XX DE Monoclonal antibody; heavy metal; mercury; variable region;

XX KM light chain.

XX OS Synthetic.

XX PN WO9520607-A.

XX PD 03-AUG-1995.

XX PF 27-JAN-1995; 95WO-US01199.

XX PR 27-JAN-1994; 94US-0187407.

XX PA (BION-) BIONEERASKA INC.

XX PI Lopez O, Wagner FW, Wylie DE;

XX DR WPI; 1995-275415/36.

XX DR N-PSDB; AAQ97508.

XX PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from

PT monoclonal antibodies, used for detecting, removing, adding or

PT neutralising heavy metals

XX PS Claim 23; Page 67-68; 106pp; English.

XX CC Hybridoma antibodies have been produced with the spleen cells of

CC BALB/c mouse that had received multiple injections of mercuric ions

CC reacted with glutathione to produce a mercuric ion coordinate

CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing MAbs that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by multi reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CH1 domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' end of  
 CC the kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AA097511-097518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer AA097518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in AA097498-097510 and the deduced AA sequences in AA879241-R79250 &  
 CC AA87970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.

CC Sequence 107 AA:

Query Match 83.9%; Score 471.5; DB 16; Length 107;  
 Best Local Similarity 83.2%; Pred. No. 1e-29;  
 Matches 89; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

OY 1 DIOMTOSSSLSASVGDYITCKTSQDINKYMWYQOTPGKAPRLIHYTSALOPGIPS 60  
 DB 1 dqlmqspsslsaslgkvltckasqdkinkylayqhpqkgrlllytsalqpsips 60  
 OY 61 RPSGSGSGRDYFTTISLOPEDATYTCLOYDNLMTFGGCTVEIK 106  
 DB 61 rfsgsgsgrdyfttislpediatytcloydnltwfggctveik 107

# RESULT 14

AA893159 standard; Protein; 108 AA.

AC AAR93159;  
 DT 24-OCT-1996 (first entry)  
 XX

DE Murine monoclonal antibody K20 kappa chain variable region.

KW Antibody; light chain; kappa; variable region; K20; Integrin; CD29;  
 KW beta 1 subunit; humanisation; Hu-K20; immunosuppressant;  
 XX T cell activation; complementarity determining region; CDR.

OS Mus musculus.

XX Key Location/Qualifiers

FT 1..23 /label= FRI

FT /note= "framework region"

FT 24..34 /label= CDR1

FT /note= "complementarity determining region"

FT 35..49 /label= FR2

FT /note= "framework region"

FT 50..56 /label= CDR2

FT /note= "complementarity determining region"

FT 57..88 /label= FR3

FT /note= "framework region"

FT 89..94 /label= CDR3

FT /note= "complementarity determining region"

FT Region 95..108  
 FT /label= J\_kappa1

PN FR2724393-A1.

PD 15-MAR-1996.

PF 12-SEP-1994; 94FR-0010858.

PR 12-SEP-1994; 94FR-0010858.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 (PROT-) PROTEINE PERFORMANCE SA.

PI Bernard A, Cervoni MF, Lefranc MP, Margatite C;

DR WPI; 1996-162083/17.

DR N-PSDB; AAT26849.

PT Humanisation of non-human immunoglobulin variable regions - for  
 PT prodn. of humanised antibodies, esp. K20, e.g. as an  
 PT immunosuppressant

XX Example 1; Fig 2A; 39pp; French.

CC The present sequence is that of the variable region of the kappa  
 CC light chain from murine monoclonal antibody K20. The antibody  
 CC recognises the beta 1 subunit (CD29) of integrins and inhibits  
 CC activation and proliferation of peripheral T cells induced by  
 CC anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target  
 CC for humanisation; the humanised version may be useful as an  
 CC immunosuppressant. In the humanisation process, the complementarity  
 CC determining regions (CDRs) of a human antibody with framework  
 CC CDRs.  
 CC regions 70-95% homologous to those of K20 were replaced by the K20  
 CC CDRs.

XX Sequence 108 AA:

Query Match 82.7%; Score 465; DB 17; Length 108;  
 Best Local Similarity 81.1%; Pred. No. 3.4e-29;  
 Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

OY 1 DIOMTOSSSLSASVGDYITCKTSQDINKYMWYQOTPGKAPRLIHYTSALOPGIPS 60  
 DB 1 dqlmqspsslsaslgkvltckasqdkinkylayqhpqkgrlllytsalqpsips 60

OY 61 RPSGSGSGRDYFTTISLOPEDATYTCLOYDNLMTFGGCTVEIK 106  
 DB 61 rfsgsgsgrdyfttislpediatytcloydnltwfggctveik 106

# RESULT 15

AA806252 standard; Protein; 128 AA.

AC AAR06252;

DT 10-DEC-1990 (first entry)

DE Variable region of murine AHT 107 light chain.

KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;

OS Mus sp.

XX EP380068-A.

XX 01-AUG-1990.

PF 24-JAN-1990; 90EP-0101351.

```

PR 04-DEC-1989; 8905-0441702.
PR 24-JAN-1989; 8905-0301216.
XX
XX (MOLE-) MOLECULAR THERAPEUT.
PA
XX
XX Zerler B;
PI
XX WPI: 1990-232892/31.
DR N-PSDB: AA005556.
XX
XX Expression vectors for producing chimeric monoclonal antibodies
PT which express human constant region and non-human variable region
XX
XX Disclosure: ; P: English.
XX
XX MAb comprising mouse CH and CL constant regions which human
CC variable regions may be used to create mouse/human hybrid Mabs,
CC which have a longer serum half-life. Method can be used to produce
CC Abs against Interleukin-2 receptor and tumour necrosis factor.
XX
SQ Sequence 128 AA:

Query Match 81.9%; Score 460.5; DB 11; Length 128;
Best Local Similarity 76.6%; Pred. No. 8,8e-29;
Matches 82; Conservative 18; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIQMTSPSSLSASVGDRTYTICTKTQDINKYMWYQOTPGKAPRLIHVTSALQPGIPS 60
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 dIqmtspsslsaslgkvtlctksqdlnkrlawyhkpggprlilnytsrlqpgips 80

OY 61 RFSGSGSGRDYTFETISSLOPEDIAITYCYDNL-WTFSGGTKEIK 106
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 rfsgsgsgkdyfslnlepediatyylrddlpwtcfgggklevr 127

```

Search completed: July 9, 2002, 15:40:36  
 Job time: 122 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: July 9, 2002, 15:38:34 ; Search time 20.73 Seconds

(without alignments)  
124.897 Million cell updates/sec

Title: US-09-010-377-1

Perfect score: 562  
Sequence: 1 D1QMTQSPSSLSASVGRVT.....YCLQYDNLMTFGQCKVEIK 106Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued\_Patents\_AA.\*  
1: /cgn2-6/plodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2-6/plodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2-6/plodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2-6/plodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2-6/plodata/2/1aa/PCUS.COMB.pep.\*  
6: /cgn2-6/plodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	106	2	US-08-561-521-7
2	562	100.0	106	5	PCT-US95-01219-7
3	508	90.4	106	2	US-08-561-521-5
4	508	90.4	106	5	PCT-US95-01219-5
5	508	90.4	126	2	US-08-561-521-2
6	508	90.4	126	2	US-08-561-521-15
7	508	90.4	126	5	PCT-US95-01219-2
8	508	90.4	126	5	PCT-US95-01219-15
9	481	85.6	128	1	US-08-339-582-4
10	471.5	83.9	107	2	US-08-888-366-22
11	460	81.9	637	1	US-08-235-838-16
12	460	81.9	637	2	US-08-465-473B-16
13	455	81.0	241	1	US-08-235-838-11
14	455	81.0	241	2	US-08-465-473B-11
15	454.5	80.9	108	2	US-08-602-725-29
16	453.5	80.7	107	2	US-08-561-521-8
17	453.5	80.7	107	5	PCT-US95-01219-8
18	451	80.2	355	3	US-08-875-811-57
19	448.5	79.8	107	2	US-07-934-373C-17
20	448.5	79.8	107	3	US-08-437-642B-17
21	448.5	79.8	107	5	PCT-US93-07832-17
22	444.5	79.1	107	2	US-07-934-373C-18
23	444.5	79.1	107	3	US-08-437-642B-18
24	444.5	79.1	107	5	PCT-US93-07832-18
25	444.5	79.1	108	3	US-08-974-899-3
26	444.5	79.1	111	1	US-08-137-117D-67
27	444.5	79.1	111	2	US-08-436-717-67

28	444.5	79.1	126	1	US-08-137-117D-71	Sequence 71, Appl
29	444.5	79.1	126	2	US-08-436-717-71	Sequence 71, Appl
30	443.5	78.9	107	2	US-08-561-521-6	Sequence 6, Appl
31	443.5	78.9	107	2	US-08-652-558-34	Sequence 34, Appl
32	443.5	78.9	107	4	US-09-025-203-15	Sequence 15, Appl
33	443.5	78.9	107	5	PCT-US95-01219-6	Sequence 6, Appl
34	443.5	78.9	108	2	US-08-070-116A-7	Sequence 7, Appl
35	443.5	78.9	108	2	US-08-116-247-9	Sequence 9, Appl
36	441.5	78.6	107	2	US-08-318-157B-6	Sequence 6, Appl
37	440.5	78.4	107	2	US-08-652-558-2	Sequence 2, Appl
38	440.5	78.4	109	2	US-07-934-373C-3	Sequence 3, Appl
39	440.5	78.4	109	5	US-08-437-642B-3	Sequence 3, Appl
40	440.5	78.4	109	5	PCT-US93-07832-3	Sequence 3, Appl
41	440.5	78.4	214	2	US-07-934-373C-39	Sequence 39, Appl
42	440.5	78.4	214	2	US-08-437-642B-39	Sequence 39, Appl
43	440.5	78.4	214	5	PCT-US93-07832-39	Sequence 39, Appl
44	438.5	78.0	107	4	US-09-254-189-1	Sequence 1, Appl
45	438.5	78.0	109	2	US-07-934-373C-47	Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-08-561-521-7  
Sequence 7, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legert, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
ADHESION MOLECULE VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend Khourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-7

Query Match 100.0% Score 562; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. NO. 1.2e-45;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCKTSODINKMAMYOOTPGKAPRLLIHYTSALQPGIPS 60  
|||||  
DB 1 DIOMTSPSSLSASVGDRTITCKTSODINKMAMYOOTPGKAPRLLIHYTSALQPGIPS 60  
|||||

QY 61 RFGSGSGRDYFTTSSLOPEDIAITYCYLOYDNMTFCGKTVEIK 106  
|||||  
DB 61 RFGSGSGRDYFTTSSLOPEDIAITYCYLOYDNMTFCGKTVEIK 106  
|||||

RESULT 2  
PCT-US95-01219-7  
Sequence 7, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCR-US95-01219-7

Query Match 100.0%; Score 562; DB 5; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.2e-45;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCKTSODINKMAMYOOTPGKAPRLLIHYTSALQPGIPS 60  
|||||  
DB 1 DIOMTSPSSLSASVGDRTITCKTSODINKMAMYOOTPGKAPRLLIHYTSALQPGIPS 60  
|||||

QY 61 RFGSGSGRDYFTTSSLOPEDIAITYCYLOYDNMTFCGKTVEIK 106  
|||||  
DB 61 RFGSGSGRDYFTTSSLOPEDIAITYCYLOYDNMTFCGKTVEIK 106  
|||||

RESULT 3  
US-08-561-521-5

Sequence 5, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-5

Query Match 90.4%; Score 508; DB 2; Length 106;  
Best Local Similarity 88.7%; Pred. No. 1.2e-40;  
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTITCKTSODINKMAMYOOTPGKAPRLLIHYTSALQPGIPS 60  
|||||  
DB 1 DIOMTSPSSLSASVGDRTITCKTSODINKMAMYOOTPGKAPRLLIHYTSALQPGIPS 60  
|||||

QY 61 RFGSGSGRDYFTTSSLOPEDIAITYCYLOYDNMTFCGKTVEIK 106  
|||||  
DB 61 RFGSGSGRDYFTTSSLOPEDIAITYCYLOYDNMTFCGKTVEIK 106  
|||||

RESULT 4  
PCT-US95-01219-5  
Sequence 5, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000



CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-5

Query Match 90.4% Score 508; DB 5; Length 106;  
Best Local Similarity 88.7% Pred. No. 1.2e-40;  
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDVRYTICKTSQDINKYMWYQTPGKAPRLLIHTSALOPGIPS 60  
DB 1 DIOMTSPSSLSASLGKVTICKTSQDINKYMWYQHKRPRLLIHTSALOPGIPS 60  
OY 61 RFGSGSGRDYFTTSSLOPEDIAITYCYQYDNLMTFGGTRLEIK 106  
DB 61 RFGSGSGRDYFTTSSLOPEDIAITYCYQYDNLMTFGGTRLEIK 106

RESULT 5  
US-08-561-521-2  
Sequence 2, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legier, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-2

Query Match 90.4% Score 508; DB 2; Length 126;  
Best Local Similarity 88.7% Pred. No. 1.5e-40;  
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDVRYTICKTSQDINKYMWYQTPGKAPRLLIHTSALOPGIPS 60  
DB 21 DIOMTSPSSLSASLGKVTICKTSQDINKYMWYQHKRPRLLIHTSALOPGIPS 80  
OY 61 RFGSGSGRDYFTTSSLOPEDIAITYCYQYDNLMTFGGTRLEIK 106  
DB 81 RFGSGSGRDYFTTSSLOPEDIAITYCYQYDNLMTFGGTRLEIK 126

RESULT 6  
US-08-561-521-15  
Sequence 15, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legier, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-15

Query Match 90.4%; Score 508; DB 2; Length 126;  
Best Local Similarity 88.7%; Pred. No. 1.5e-40;  
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTTCTKTSODINKYMWYQOTPGKAPRLLIHTSALQPGIPS 60  
|||||  
DB 21 DIQMTSPSSLSASLGKVTITCKTSODINKYMWYQHKGKRPRLLIHTSALQPGIPS 80  
|||||

OY 61 RFGSGSGRDYTFITSSLOPEDIAITYYCLOYDNIMTFGGTKLEIK 106  
|||||  
DB 81 RFGSGSGRDYTFITSSLOPEDIAITYYCLOYDNIMTFGGTKLEIK 126  
|||||

## RESULT 7

PCT-US95-01219-2  
Sequence 2, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-2

Query Match 90.4%; Score 508; DB 5; Length 126;  
Best Local Similarity 88.7%; Pred. No. 1.5e-40;  
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTTCTKTSODINKYMWYQOTPGKAPRLLIHTSALQPGIPS 60  
|||||  
DB 21 DIQMTSPSSLSASLGKVTITCKTSODINKYMWYQHKGKRPRLLIHTSALQPGIPS 80  
|||||

OY 61 RFGSGSGRDYTFITSSLOPEDIAITYYCLOYDNIMTFGGTKLEIK 106  
|||||  
DB 81 RFGSGSGRDYTFITSSLOPEDIAITYYCLOYDNIMTFGGTKLEIK 126  
|||||

## RESULT 8

PCT-US95-01219-15  
Sequence 15, Application PC/TUS9501219  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Leger, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VLA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01219  
FILING DATE: 25-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/186,269  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-01219-15

Query Match 90.4%; Score 508; DB 5; Length 126;  
Best Local Similarity 88.7%; Pred. No. 1.5e-40;  
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTTCTKTSODINKYMWYQOTPGKAPRLLIHTSALQPGIPS 60  
|||||  
DB 21 DIQMTSPSSLSASLGKVTITCKTSODINKYMWYQHKGKRPRLLIHTSALQPGIPS 80  
|||||

OY 61 RFGSGSGRDYTFITSSLOPEDIAITYYCLOYDNIMTFGGTKLEIK 106  
|||||  
DB 81 RFGSGSGRDYTFITSSLOPEDIAITYYCLOYDNIMTFGGTKLEIK 126  
|||||

## RESULT 9

US-08-339-582-4  
Sequence 4, Application US/08339582  
Patent No. 5558852  
GENERAL INFORMATION:  
APPLICANT: Bigner, Darrell D.  
APPLICANT: Zalusky, Michael R.  
APPLICANT: Carrel, Stefan

TITLE OF INVENTION: METHOD OF TREATMENT  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley  
STREET: P.O. Drawer 34009  
CITY: Charlotte  
STATE: No. 5558852th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/339,582  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/033,864  
FILING DATE: 19-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5405-89  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-339-582-4

Query Match 85.6%; Score 481; DB 1; Length 128;  
Best Local Similarity 84.0%; Pred. NO. 4.9e-38;  
Matches 89; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Db 1 DIOMTQSPSSLSASVGDRTVTITCKTSODINKYMAWYQOTPGKAPRLDIHTSALQPGIPS 60  
1 DIOMTQSPSSLSASLGKVTITCKASODINKYIAWQHKGKGRLLIHTSTLQPGIPS 80

QY 61 RFGSGSGRDYPTFTISLQPDIAITYCLOYDNLTGCGTKVEIK 106  
1 RFGSGSGRDYFSISINPEPDIAITYCLOYDNLTGCGTKLEIK 126

Db 81 RFGSGSGRDYFSISINPEPDIAITYCLOYDNLTGCGTKLEIK 126

RESULT 10  
US-08-888-366-22  
Sequence 22, Application US/08888366  
Patent No. 5972656  
GENERAL INFORMATION:  
APPLICANT: Lopez, Osvaldo  
APPLICANT: Wylie, Dwane E.  
APPLICANT: Wagner, Fred W.  
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,366  
FILING DATE: 03-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,407  
FILING DATE: 27-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,542  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/493,299  
FILING DATE: 14-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/324,392  
FILING DATE: 14-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648,39USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-22

Query Match 83.9%; Score 471.5; DB 2; Length 107;  
Best Local Similarity 83.2%; Pred. No. 3.1e-37;  
Matches 89; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIOMTQSPSSLSASVGDRTVTITCKTSODINKYMAWYQOTPGKAPRLDIHTSALQPGIPS 60  
1 DIOMTQSPSSLSASLGKVTITCKASODINKYIAWQHKGKGRLLIHTSTLQPGIPS 60

Db 61 RFGSGSGRDYPTFTISLQPDIAITYCLOYDNLTGCGTKVEIK 106  
61 RFGSGSGRDYFSISINPEPDIAITYCLOYDNLTGCGTKLEIK 107

Db 61 RFGSGSGRDYPTFTISLQPDIAITYCLOYDNLTGCGTKVEIK 106  
61 RFGSGSGRDYFSISINPEPDIAITYCLOYDNLTGCGTKLEIK 107

RESULT 11  
US-08-235-838-16  
Sequence 16, Application US/08235838  
Patent No. 5571894  
GENERAL INFORMATION:  
APPLICANT: Wels, Winfried S.  
APPLICANT: Hynes, Nancy E.  
APPLICANT: Harwerth, Ina-Maria  
APPLICANT: Groner, Bernd  
APPLICANT: Hardman, No. 5571894man  
TITLE OF INVENTION: Recombinant Antibodies Specific for a  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,838  
FILING DATE: TBA



LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-235-838-11

Query Match  
Best Local Similarity 81.0%; Score 455; DB 1; Length 241;  
Matches 84; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITCKTSODINKYAMWQOFGKAPRLIHYSALQPGIPS 60  
DB 137 DIQMTSPSSLSASVGDRTITCKTSODINKYAMWQOFGKAPRLIHYSALQPGIPS 196  
DB 197 RFGSGSGRDYFTTSSLOPEDATYCCLOYDNLMTFGGCTKVEI 105  
197 RFGSGSGRDYFTTSSLOPEDATYCCLOYDNLMTFGGCTKLEI 241

RESULT 14  
US-08-465-473B-11  
Sequence 11, Application US/08465473B  
Patent No. 5939531  
GENERAL INFORMATION:  
APPLICANT: Weis, Winfried S.  
APPLICANT: Hynes, Nancy E.  
APPLICANT: Harwerth, Ina-Marie  
APPLICANT: Groner, Bernd  
APPLICANT: Hardman, No. 5939531man  
APPLICANT: Zwickl, Markus  
TITLE OF INVENTION: Recombinant Antibodies Specific for a  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NOVARTIS Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901-6940  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,473B  
FILING DATE: 5 June 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/828,832  
FILING DATE: 31-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 91-810079.3  
FILING DATE: 05-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pfeiffer, Henna J.  
REGISTRATION NUMBER: 22,640  
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)522 6940  
TELEFAX: (908)522 6955  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-465-473B-11

Query Match 81.0%; Score 455; DB 2; Length 241;

Best Local Similarity 80.0%; Pred. No. 2,6e-35;  
Matches 84; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITCKTSODINKYAMWQOFGKAPRLIHYSALQPGIPS 60  
DB 137 DIQMTSPSSLSASVGDRTITCKTSODINKYAMWQOFGKAPRLIHYSALQPGIPS 196  
DB 197 RFGSGSGRDYFTTSSLOPEDATYCCLOYDNLMTFGGCTKVEI 105  
197 RFGSGSGRDYFTTSSLOPEDATYCCLOYDNLMTFGGCTKLEI 241

RESULT 15  
US-08-602-725-29  
Sequence 29, Application US/08602725  
Patent No. 5965710  
GENERAL INFORMATION:  
APPLICANT: BODMER, WALTER F  
APPLICANT: DURBIN, HELGA  
APPLICANT: SNARY, DAVID  
APPLICANT: STEWART, LORNA MD  
APPLICANT: YOUNG, SUSAN  
APPLICANT: BATES, PAUL A  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHUE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,725  
FILING DATE: 02-FEB-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB94/01816  
FILING DATE: 19-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9317423  
FILING DATE: 21-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 1090-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4091  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: HUKAN REI light chain  
US-08-602-725-29

Query Match 80.9%; Score 454.5; DB 2; Length 108;  
Best Local Similarity 83.0%; Pred. No. 1.2e-35;  
Matches 88; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

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Page 8

Qy 1 DIQMTQSPSSLSASVGDPRVTITCKTSODINKYMAWYOOTPGKAPRLIHTYSALQPGIPS 60  
Db 1 DIQMTQSPSSLSASVGDPRVTITCKTSODINKYMAWYOOTPGKAPRLIHTYSALQPGIPS 60  
Qy 61 RFGSGSGRDTFTTSSIQPEDIATYCYCLOYDNL-WTFGGTKVEI 105  
Db 61 RFGSGSGRDTFTTSSIQPEDIATYCYCLOYDNL-WTFGGTKVEI 106

Search completed: July 9, 2002, 15:39:04  
Job time: 30 sec



A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se  
 A:Reference number: S07453; MUID:83058021  
 A:Accession: S07453  
 A:Molecule type: protein  
 A:Residues: 1-43 <ROC2>  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotetramer; Immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 72.8%; Score 477; DB 2; Length 120;  
 Matches 93; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKSCASGFINIKDTYIHVWROAPGRLMGMGRIPANGYTKY 60  
 Db 1 EVQLDQSGAEVKKPGASVKSLKSTCASTGYNIDYTHHWKQKPGQGLEWGMGRIIPANGYTKY 60  
 QY 61 DPKFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 120  
 Db 61 DPKFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 120  
 QY 121 VSS 123  
 Db 117 VSS 119

## RESULT 3

Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
 C:Accession: S36265  
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36265; MUID:93178448  
 A:Accession: S36265  
 A:Status: Preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <GR1>  
 A:Cross-references: EMBL:218846; NID:933121; PIDN:CAA79298.1; PID:9339900  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotetramer; Immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 72.3%; Score 473.5; DB 2; Length 118;  
 Matches 96; Conservative 6; Mismatches 13; Indels 11; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKSCASGFINIKDTYIHVWROAPGRLMGMGRIPANGYTKY 60  
 Db 1 QVQLVSGAEVKKPGASVKSCASGFTFTYTHHWKQKPGQGLEWGMGRIIPANGYTKY 60  
 QY 61 DPKFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 117  
 Db 61 ADFFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 117  
 QY 118 LTVVSS 123  
 Db 113 LTVVSS 118

## RESULT 4

Ig heavy chain V-1 region (W12) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
 C:Accession: D33548  
 R:Kipp, J.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp

A:Reference number: A33548; MUID:89345575  
 A:Accession: D33548  
 A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <RIP>  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotetramer; Immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 71.5%; Score 468; DB 2; Length 123;  
 Matches 92; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKSCASGFINIKDTYIHVWROAPGRLMGMGRIPANGYTKY 60  
 Db 1 QVQLVSGAEVKKPGASVKSCASGFTFTYTHHWKQKPGQGLEWGMGRIIPANGYTKY 60  
 QY 61 DPKFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 120  
 Db 61 ADFFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 120  
 QY 121 VSS 123  
 Db 121 VSS 123

## RESULT 5

Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Aug-1996  
 C:Accession: A32483  
 R:Larlick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck  
 A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells  
 A:Reference number: A32483; MUID:89273586  
 A:Accession: A32483  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-142 <LAR>  
 A:Cross-references: GB:M26463  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotetramer; Immunoglobulin  
 F:25-108/Domain: Immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 71.3%; Score 467; DB 2; Length 142;  
 Matches 93; Conservative 8; Mismatches 22; Indels 4; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKSCASGFINIKDTYIHVWROAPGRLMGMGRIPANGYTKY 60  
 Db 11 QVQLVSGAEVKKPGASVKSCASGFTFTYTHHWKQKPGQGLEWGMGRIIPANGYTKY 60  
 QY 61 DPKFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 70  
 Db 71 ADFFGGRVITADTSASTAYMELSLRSEDTAVYCARREGYGYNGVYAMDYWGQGLVT 116  
 QY 117 LTVVSS 123  
 Db 131 LTVVSS 137

## RESULT 6

Ig heavy chain V region (E8) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S17586  
 R:Myldgaard, S.E.; Paterson, Y.; Kaiser, K.; Bowdlish, K.; Getzoff, E.D.  
 A:Title: Biochemical implications from the variable gene sequences of an anti-cytochr



100

1



Db 20 QVQLVSGAEVKKPGASVKVSCKASGTFSTGYTHHWRAAPGQGLEMMGWINPNSGCTNY 79  
 QY 61 DPKFGGRVITADTSASTAVMELSLRSEDPAVYVC--AREGYGNVCYVAMDYWGQGL 118  
 Db 80 AOKFGGRVITADTSASTAVMELSLRSEDPAVYVCARCY-----NYWGQGL 130  
 QY 119 VTSS 123  
 Db 131 VTSS 135

## RESULT 14

S03484  
 19 heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 A:Variety: Strain BALB/c  
 C:Date: 26-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 21-Jan-2000  
 C:Accession: S03484; S07453  
 R:Rocca-Serra, J.; Maches, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.  
 EMBL J. 2, 867-872, 1983  
 A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT  
 hypervariable regions.  
 A:Reference number: S03471; MUID:84057768  
 A:Accession: S03484  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 10-120 <R0C1>  
 A:Cross-references: EMBL:X07144  
 A:Note: This sequence was determined from the differentiated gene  
 R:Rocca-Serra, J.; Mazie, J.C.; Moliner, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere  
 J. Immunol. 129, 2554-2558, 1982  
 A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se  
 A:Reference number: S07453; MUID:83058021  
 A:Accession: S07453  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-43 <R0C2>  
 C:Superfamily: immunoglobulin V region: immunoglobulin homology  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 447; DB 2; Length 120;  
 Best Local Similarity 71.5%; Pred. No. 4.2e-33;  
 Matches 88; Conservative 11; Mismatches 20; Indels 4; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGTFSTGYTHHWRAAPGQGLEMMGWINPNSGCTNY 60  
 Db 1 EYQLVSGAEVKKPGASVKVSCKASGTFSTGYTHHWRAAPGQGLEMMGWINPNSGCTNY 60  
 QY 61 DPKFGGRVITADTSASTAVMELSLRSEDPAVYVCAREGYGNVCYVAMDYWGQGL 120  
 Db 61 GPKFGGRVITADTSASTAVMELSLRSEDPAVYVCAREGYGNVCYVAMDYWGQGL 116  
 QY 121 VSS 123  
 Db 117 VSS 119

## RESULT 15

PH0960  
 19 heavy chain V region (G6+ T-L30) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0960  
 R:Martin, T.; Dufy, S.F.; Carson, D.A.; Kippes, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A:Title: Evidence for somatic selection of natural autoantibodies.  
 A:Reference number: PH0952; MUID:92202880  
 A:Accession: PH0960  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-136 <MAR>  
 C:Superfamily: immunoglobulin V region: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-124/Region: complementarity-determining 3

Query Match 68.2%; Score 446.5; DB 2; Length 136;  
 Best Local Similarity 69.1%; Pred. No. 5.3e-33;  
 Matches 94; Conservative 1; Mismatches 28; Indels 13; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGTFSTGYTHHWRAAPGQGLEMMGWINPNSGCTNY 60  
 Db 1 EYQLVSGAEVKKPGASVKVSCKASGTFSTGYTHHWRAAPGQGLEMMGWINPNSGCTNY 60  
 QY 61 DPKFGGRVITADTSASTAVMELSLRSEDPAVYVCAREGYGNVCYVAMDYWGQGL 107  
 Db 61 AOKFGGRVITADTSASTAVMELSLRSEDPAVYVCAREGYGNVCYVAMDYWGQGL 120  
 QY 108 YAMDYWGQGLTVSS 123  
 Db 121 YGMDYWGQGLTVSS 136

Search completed: July 9, 2002, 15:39:38  
 Job time: 64 sec

Tue Jul 9 15:50:39 2002

us-09-010-377-2.rpt

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:45:57 ; Search time 15.81 Seconds

(without alignments)  
301.234 Million cell updates/sec

Title: US-09-010-377-2

Sequence: 1 OVALVOSGAEEVKKPCASVAV.....NYGYAMDYWGCTLTAVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	427.5	65.3	147	1	HVIC_HUMAN
2	409	62.4	120	1	HV03_MOUSE
3	408.5	62.4	139	1	HV07_MOUSE
4	405	61.8	117	1	HV18_HUMAN
5	399	60.9	140	1	HV02_MOUSE
6	396	60.5	117	1	HVIC_HUMAN
7	390	59.5	117	1	HV1A_HUMAN
8	378	57.7	117	1	HV13_MOUSE
9	375.5	56.9	117	1	HV12_MOUSE
10	373	56.7	137	1	HV11_MOUSE
11	371.5	56.7	137	1	HV11_MOUSE
12	369	56.3	138	1	HV48_MOUSE
13	364.5	55.6	120	1	HV50_MOUSE
14	360	55.0	121	1	HV01_MOUSE
15	360	55.0	136	1	HV15_MOUSE
16	355	54.2	125	1	HV1F_HUMAN
17	349.5	53.4	120	1	HV1H_HUMAN
18	349	53.3	117	1	HV09_MOUSE
19	344.5	52.6	114	1	HV00_MOUSE
20	338	51.6	117	1	HV04_MOUSE
21	336	51.3	117	1	HV06_MOUSE
22	333.5	50.9	136	1	HV16_MOUSE
23	333	50.8	117	1	HV10_MOUSE
24	330.5	50.5	124	1	HV1E_HUMAN
25	329	50.2	117	1	HV14_MOUSE
26	329	50.2	117	1	HV14_MOUSE
27	326	49.8	117	1	HV49_MOUSE
28	326	49.8	117	1	HV49_MOUSE
29	325.5	49.7	119	1	HV24_MOUSE
30	324.5	49.7	124	1	HV1D_HUMAN
31	324.5	49.5	119	1	HV38_MOUSE
32	323.5	49.4	119	1	HV40_MOUSE
33	320.5	48.9	122	1	HV3G_HUMAN

## ALIGNMENTS

RESULT	ID	HVIC_HUMAN	STANDARD	PRT	147 AA
34	319	48.7	117	1	HV42_MOUSE
35	318.5	48.6	122	1	HV3A_HUMAN
36	318	48.5	121	1	HV33_HUMAN
37	317	48.4	123	1	HV19_MOUSE
38	315	48.1	123	1	HV18_MOUSE
39	314.5	48.0	122	1	HV21_MOUSE
40	314	47.9	117	1	HV05_MOUSE
41	313	47.8	123	1	HV25_MOUSE
42	313	47.8	142	1	HV01_RAT
43	312	47.6	118	1	HV39_MOUSE
44	312	47.6	123	1	HV22_MOUSE
45	311.5	47.6	122	1	HV3H_HUMAN

RESULT	1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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DB	QY	DB	QY
80	116	140	147
APRFGRTYTRRDSFSTAYMDLRSLRSDBSAVFYCAKASDPFMSDYDYNFDVSYTLVDWGQ	GLVTVVSS	GLVTVVSS	GLVTVVSS
138	123	147	147

RESULT	2	
HV03_MOUSE		
ID HV03_MOUSE	STANDARD;	PRT; 120 AA

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 heavy chain V region 36-65.  
 DE Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Crenilata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 NCBI\_TaxID=10090;

Query Match	62.4%;	Score 409;	DB 1;	Length 120;
Best Local Similarity	63.1%;	Pred. No. 3.5e-34;		
Matches 77;	Conservative 18;	Mismatches 25;	Indels 2;	Gaps 1

[illegible]

RESULT	3
HV07_MOUSE	
ID	HV07_MOUSE
AC	P01751; P01752; STANDARD; PRT; 139 AA.
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig heavy chain V region B1-8/186-2 precursor.
OS	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;
RN	[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6;  
RX MEDLINE-81234546; PubMed=6788376;  
RA Hochwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajeswsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN mRNA WAS CLODED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
-----

Query Match	62.48;	Score 408.5;	DB 1;	Length 139;
Best Local Similarity	62.68;	Pred. No. 4.7e-34;		
Matches 77: Conservative	18;	Mismatches 25;	Indels 3;	Gaps 1

[illegible]

RESULT	4
HVIB_HUMAN	
ID	HVIB_HUMAN
AC	P01743;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig heavy chain V-I region H83 precursor.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID	9606;
FN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=83144028; PubMed=6298778;

RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;  
 RT "Evolutionary aspects of Immunoglobulin heavy chain variable region  
 (VH) gene subgroups.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).  
 CC -----  
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 CC -----  
 DR EMBL: J00240; AAA52988.1;  
 DR PIR: A02024; HYH0MC.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR InterPro: IPR003596; 1g\_V.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; 1g; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL  
 FT CHAIN 1 19  
 FT NON\_TER 20 117 IG HEAVY CHAIN V-1 REGION HC3.  
 FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 61.88; Score 405; DB 1; Length 117;  
 Best Local Similarity 79.6%; Pred. No. 8.6e-34;  
 Matches 78; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

OY 1 OVOLVSGAEVKKPGASVSKASGPNIKDTYIHVWROAPGQRLKMGIDPANGYTRY 60  
 ID HV02\_MOUSE STANDARD; PRT; 140 AA.  
 AC P01746;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 1g heavy chain V region 93G7 precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A/J;  
 RX MEDLINE=82152818; PubMed=6801765;  
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
 RA Capra J.D.;  
 RT "Somatic mutation in genes for the variable portion of the  
 RT immunoglobulin heavy chain";  
 RL Science 216:309-311(1982).  
 CC -----  
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 CC -----  
 DR EMBL: J00493; AAA38128.1;  
 DR PIR: A02028; HVMSG7.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR InterPro: IPR003596; 1g\_V.

DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; 1g; 1.  
 KM Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.  
 FT SIGNAL  
 FT CHAIN 1 19  
 FT NON\_TER 20 117 IG HEAVY CHAIN V REGION 93G7.  
 FT SEQUENCE 140 AA; 15514 MW; 25A4CB8E31DA5CE8 CRC64;

Query Match 60.9%; Score 399; DB 1; Length 140;  
 Best Local Similarity 61.0%; Pred. No. 4.2e-33;  
 Matches 75; Conservative 19; Mismatches 27; Indels 2; Gaps 1;

OY 1 OVOLVSGAEVKKPGASVSKASGPNIKDTYIHVWROAPGQRLKMGIDPANGYTRY 60  
 ID HV1G\_HUMAN STANDARD; PRT; 117 AA.  
 AC P23083;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 1g heavy chain V-1 region V35 precursor.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=88296408; PubMed=2841108;  
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,  
 RA Ohno H., Fukuhara S., Honjo T.;  
 RT "Dispersed localization of D segments in the human immunoglobulin  
 RT heavy-chain locus";  
 RL EMBO J. 7:1047-1051(1988).  
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 CC -----  
 DR EMBL: X07448; -, NOT\_ANNOTATED\_CDS.  
 DR PIR: S00476; HVH035.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR InterPro: IPR003596; 1g\_V.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; 1g; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL  
 FT CHAIN 1 19  
 FT NON\_TER 20 117 IG HEAVY CHAIN V-1 REGION V35.  
 FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 60.5%; Score 396; DB 1; Length 117;  
 Best Local Similarity 78.6%; Pred. No. 6.8e-33;  
 Matches 77; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 OVOLVSGAEVKKPGASVSKASGPNIKDTYIHVWROAPGQRLKMGIDPANGYTRY 60

DB 20 QVOLVSGAEVKKPGASVSKASGYTTGTGYMHVRAPOGLFEMGRINPNSGGTNY 79  
 QY 61 DKFOGRTVITADTSASTAYMELSLRSDTAIVYCAR 98  
 DB 80 AOKFOGRTVITADTSASTAYMELSLRSDTAIVYCAR 117

RESULT 7  
 ID HV1A\_HUMAN STANDARD: PRT; 117 AA.  
 AC P01742;  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-I region EU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71064024; PubMed=5489771;  
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
 RA Waxdal M.J., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4."  
 RL Biochemistry 9:3161-3170(1970).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intra-chain disulfide bonds."  
 RL Biochemistry 9:3188-3196(1970).  
 CC -I- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS  
 CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
 CC PIR: A0203; G1HUEU.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 22 96  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEHD52818 CRC64;

Query Match 59.5%; Score 390; DB 1; Length 117;  
 Best Local Similarity 68.3%; Pred. No. 2, 7e-32;  
 Matches 84; Conservative 8; Mismatches 25; Indels 6; Gaps 2;  
 QY 1 QVOLVSGAEVKKPGASVSKASGFNFKDTYIHVRAPOGLFEMGRIDPANGYTKY 60  
 DB 1 QVOLVSGAEVKKPGASVSKASGFNFKDTYIHVRAPOGLFEMGRIDPANGYTKY 60  
 QY 61 DKFOGRTVITADTSASTAYMELSLRSDTAIVYCARGGYGNVGYAMDVGQGLTVT 120  
 DB 61 AOKFOGRTVITADTSASTAYMELSLRSDTAIVYCARGGYGNVGYAMDVGQGLTVT 114  
 QY 121 VSS 123  
 DB 115 VSS 117  
 RESULT 8  
 ID HV13\_MOUSE STANDARD: PRT; 117 AA.  
 AC P01757;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region J558.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80078170; PubMed=6765983;  
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
 RT rearrangements in heavy chain V-region gene segments."  
 RL Nature 283:35-40(1980).  
 CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
 CC WHICH OCCUR IN THE D AND J SEGMENTS.  
 CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
 DR PIR: A26242; MHMSJ5.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 22 96  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 57.7%; Score 378; DB 1; Length 117;  
 Best Local Similarity 58.5%; Pred. No. 4, 3e-31;  
 Matches 72; Conservative 20; Mismatches 25; Indels 6; Gaps 1;

QY 1 QVOLVSGAEVKKPGASVSKASGFNFKDTYIHVRAPOGLFEMGRIDPANGYTKY 60  
 DB 1 EYQIQSGPELVKPGASVSKASGYTFETDYMKVKVSHGSKSLWIGIDINPNNGTSY 60  
 QY 61 DKFOGRTVITADTSASTAYMELSLRSDTAIVYCARGGYGNVGYAMDVGQGLTVT 120  
 DB 61 NOKFKGKATLVTKSSSTAYMQLNSLTSDSAVYCYCARDRY-----WYFDWAGTIVT 114  
 QY 121 VSS 123  
 DB 115 VSS 117  
 RESULT 9  
 ID HV51\_MOUSE STANDARD: PRT; 118 AA.  
 AC P06330;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region AC38 205.12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=84182519; PubMed=6201362;  
 RA Dildrop R., Bovens J., Silekewitz M., Beyreuther K., Rajewsky K.;  
 RT "A V region determinant (idiotope) expressed at high frequency in B  
 RT lymphocytes is encoded by a large set of antibody structural genes."  
 RL EMBO J. 3:517-523(1984).  
 DR PIR: A02040; MHMS38.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 98  
 FT DOMAIN 99 104  
 FT DOMAIN 105 118  
 FT DISULFID 22 96  
 BY SIMILARITY.



FT NON\_TER 118 118  
SQ SEQUENCE 118 AA: 12934 MW: 94F7BEAC762A018 CRC64:

Query Match 57.3%: Score 375.5; DB 1; Length 118;  
Best Local Similarity 58.5%: Pred. No. 7.7e-31;  
Matches 72; Conservative 17; Mismatches 29; Indels 5; Gaps 1;

OY 1 QVQVOSGAEVKKPPGASVYVSCASGAFNKTDTYIMHWROAPQORLEMMGRIDPANGYTKY 60  
DB 1 EVQLOOSGPELVKPGASVYVSCASGAFNKTDTYIMHWROAPQORLEMMGRIDPANGYTKY 60  
OY 61 DPKFGQRTVITADTSASTAYMELSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 120  
DB 61 NOKFKKATLTVDKSSSTAYMELSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 115  
OY 121 VSS 123  
DB 116 VSS 118

RESULT 10  
HV12\_MOUSE STANDARD; PRT; 117 AA.

ID HV12\_MOUSE  
AC P01755:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 1g heavy chain V region MOPC 104E.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83075344; PubMed=6816276;  
RA Kenly M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
Hood L.E.;  
RT "Complete amino acid sequence of a mouse mu chain: homology among  
heavy chain constant region domains.";  
RL Biochemistry 21:5415-5424(1982).  
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA  
PROTEIN HAS ALSO BEEN DETERMINED.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
DR PIR: A02039; MIMSAE.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR SMART: PF00047; 1g; 1.  
DR SMART: SM00406; 1g\_V.  
KW Immunoglobulin V region; glycoprotein.  
FT DISULFID 22 96 BY SIMILARITY.  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA: 12983 MW: 3CF8ACE4BE47E41 CRC64:

Query Match 56.9%: Score 373; DB 1; Length 117;  
Best Local Similarity 59.3%: Pred. No. 1.4e-30;  
Matches 73; Conservative 19; Mismatches 25; Indels 6; Gaps 2;

OY 1 QVQVOSGAEVKKPPGASVYVSCASGAFNKTDTYIMHWROAPQORLEMMGRIDPANGYTKY 60  
DB 1 EVQLOOSGPELVKPGASVYVSCASGAFNKTDTYIMHWROAPQORLEMMGRIDPANGYTKY 60  
OY 61 DPKFGQRTVITADTSASTAYMELSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 120  
DB 61 NOKFKKATLTVDKSSSTAYMELSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 114  
OY 121 VSS 123  
DB 115 VSS 117

RESULT 11  
HV11\_MOUSE STANDARD; PRT; 137 AA.

ID HV11\_MOUSE  
AC P01755:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 1g heavy chain V region S43 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81234548; PubMed=6788376;  
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
Baltimore D.;  
RT "Heavy chain variable region contribution to the NPB family of  
antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
(NPB ANTIBODIES).  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: J00539; AAA38172.1; .  
DR PIR: A02038; G2MS43.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR PIR: PF00047; 1g; 1.  
DR SMART: SM00406; 1g; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 122 D SEGMENT.  
FT DOMAIN 123 137 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA: 15200 MW: ADD5881BF44B8EC9 CRC64:

Query Match 56.7%: Score 371.5; DB 1; Length 137;  
Best Local Similarity 60.2%: Pred. No. 2.3e-30;  
Matches 74; Conservative 14; Mismatches 30; Indels 5; Gaps 2;

OY 1 QVQVOSGAEVKKPPGASVYVSCASGAFNKTDTYIMHWROAPQORLEMMGRIDPANGYTKY 60  
DB 20 QVQLOOPGAEVKKPPGASVYVSCASGAFNKTDTYIMHWROAPQORLEMMGRIDPANGYTKY 79  
OY 61 DPKFGQRTVITADTSASTAYMELSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 120  
DB 80 NEHFRKATLTVDKSSSTAYMELSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 134  
OY 121 VSS 123  
DB 135 VSS 137

RESULT 12  
HV48\_MOUSE STANDARD; PRT; 138 AA.

ID HV48\_MOUSE

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AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DR InterPro: IPR003006; Ig_MHC.
DE 15-JUL-1999 (Rel. 38, Last sequence update)
DE Ig heavy chain V region TREC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84248078; PubMed=6429663;
RX Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HMMST7.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 138
FT DOMAIN 21 138 IG HEAVY CHAIN V REGION TREC 1017
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 56.3%; Score 369; DB 1; Length 138;
Best Local Similarity 58.1%; Pred. No. 4,1e-30;
Matches 72; Conservative 20; Mismatches 26; Indels 6; Gaps 2;

QY 1 QVQLVDSGAEVKKPKASVSKASGKSGFNKIDTYIHWRQAGORLEMMGRIDPANGTYKY 60
DB 20 QVQLVDSGAEVKKPKASVSKASGKSGFNKIDTYIHWRQAGORLEMMGRIDPANGTYKY 79
QY 61 DPKRGVTTTADTSASTAYWELSLRSEDTAVYYCAR-EGYNGYGVYADYWGQGLTV 119
DB 80 NEKFKKATLTIVDKSSSTAYWQLSLTPPEFAVYYCARSDGYDWF-----VWVGQGLTV 134
QY 120 TVSS 123
DB 135 TFSA 138

RESULT 13
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84182519; PubMed=6201362;
RX Dildrop R., Borens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RA "A V region determinant (idiotype) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).

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DR PIR: A02037; MMS15.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR Immunoglobulin V region.
FT CHAIN 1 98
FT DOMAIN 99 105 V SEGMENT.
FT DOMAIN 106 120 D SEGMENT.
FT DISULFID 22 96 J SEGMENT.
FT NON_TER 120 120 BY SIMILARITY.
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 55.6%; Score 364.5; DB 1; Length 120;
Best Local Similarity 56.1%; Pred. No. 9,8e-30;
Matches 69; Conservative 19; Mismatches 32; Indels 3; Gaps 1;

QY 1 QVQLVDSGAEVKKPKASVSKASGKSGFNKIDTYIHWRQAGORLEMMGRIDPANGTYKY 60
DB 1 QVQLVDSGAEVKKPKASVSKASGKSGFNKIDTYIHWRQAGORLEMMGRIDPANGTYKY 60
QY 61 DPKRGVTTTADTSASTAYWELSLRSEDTAVYYCAR-EGYNGYGVYADYWGQGLTV 120
DB 61 NEKFKKATLTIVDKSSSTAYWQLSLTPPEFAVYYCARSDGYDWF-----VWVGQGLTV 117
QY 121 VSS 123
DB 118 VSS 120

RESULT 14
HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=81053741; PubMed=6253904;
RX Zakut R., Cohen J., Givol D.;
RA "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11."
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR: A02027; GYMS11.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED08F CRC64;

Query Match 55.0%; Score 360; DB 1; Length 121;
Best Local Similarity 55.3%; Pred. No. 2,8e-29;
Matches 68; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 1 QVQLVDSGAEVKKPKASVSKASGKSGFNKIDTYIHWRQAGORLEMMGRIDPANGTYKY 60
DB 1 EAQLOOQSGAEIVKPGTSVKISKAGAGTYFTYWGWERKRGHLEWIGDIYPGCGFTNY 60

```

QY 61 DPKFGRTTADTSASTAVNELSLRSEDTAVYYCAREGYGNYGAYAMDYMGCTLT 120  
Db 61 NDNKKGKATLTADTSASTAVNELSLRSEDTAVYYCAREGYGNYGAYAMDYMGCTLT 118  
QY 121 VSS 123  
Db 119 VSS 121

Job time: 373 sec

RESULT 15  
HVL5\_MOUSE  
ID HVL5\_MOUSE STANDARD; PRT: 136 AA.  
AC P01759:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 19 heavy chain V region BCL1 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82222262; PubMed=6806821;  
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,  
RA Blattner F.R.;  
RT \*Simultaneous expression of immunoglobulin mu and delta heavy chains  
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared  
RT by two adjacent CH genes.\*  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).  
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CC -----  
CC EMBL: J00494; AAA8130.1; -  
DR PIR: A02042; HVM5B1.  
DR HSSP: P01772; ZFH4.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IGV; 1.  
KM Immunoglobulin V region: Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.  
FT NON\_TER 136 136  
SQ SEQUENCE 136 AA: 15078 MM: 6827CFBC6DB3F35E CRC64;

Query Match 55.0%; Score 360; DB 1; Length 136;  
Best Local Similarity 56.9%; Pred. No. 3.2e-29;  
Matches 70; Conservative 17; Mismatches 30; Indels 6; Gaps 2;

QY 1 OYOLVSGAEYKRRGASVSKASGKFNKDTYTHWVROAPGQRLQEMGRIDPANGYTKY 60  
Db 20 OYOLVSGAEYKRRGASVSKASGKFNKDTYTHWVROAPGQRLQEMGRIDPANGYTKY 60  
QY 61 DPKFGRTTADTSASTAVNELSLRSEDTAVYYCAREGYGNYGAYAMDYMGCTLT 120  
Db 80 NDKKKGKATLTADTSASTAVNELSLRSEDTAVYYCAREGYGNYGAYAMDYMGCTLT 118  
QY 121 VSS 123  
Db 134 VSS 136

Search completed: July 9, 2002, 15:45:57

Tue Jul 9 15:50:40 2002

us-09-010-377-2.rsp

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OM protein - protein search, using sw model

Run on: July 9, 2002, 15:45:35 ; Search time 43.02 Seconds

(without alignments)  
494.616 Million cell updates/sec

Title: US-09-010-377-2

Perfect score: 1 QVQLVSGAEVKKPKASVAVK.....NGCVYAMDYGCTLTAVSS 123

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:19:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_OHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEA:19:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	457.5	69.8	124	4	09U192
2	440.5	67.3	159	4	09G050
3	440	67.2	468	11	09U131
4	432	66.0	109	11	09U185
5	432	66.0	119	4	09U194
6	432	66.0	614	4	09G0A6
7	428	65.3	119	5	09GYZ2
8	428	65.3	125	4	09U195
9	427	65.2	146	11	09U2A3
10	422	64.4	473	11	09U184
11	415.5	63.4	145	11	09U2A4
12	415.5	63.4	145	11	09U2A4
13	412	62.9	146	11	09U2A8
14	411.5	62.8	116	4	09U189
15	409.5	62.5	145	11	09U2A6
16	408.5	62.4	145	11	09U2A7

17	408.5	62.4	473	11	09U125
18	408	62.3	142	11	09U2A1
19	407.5	62.2	143	11	09U2A9
20	407	62.1	117	11	09U2A9
21	405.5	61.9	145	11	09U2A9
22	405	61.8	140	11	09U2A2
23	403.5	61.6	143	11	09U2A0
24	403.5	61.6	145	11	09U2A7
25	399	60.9	142	11	09U2A2
26	399	60.9	150	4	09U2A8
27	398.5	60.8	500	4	09U2A8
28	398	60.8	481	11	09U1T1
29	394.5	60.2	143	11	09U2A7
30	393.5	59.1	145	11	09U2A3
31	391.5	59.8	488	11	09U1R1
32	389.5	59.5	137	11	09U2A6
33	389.5	59.5	137	11	09U2A6
34	388.5	59.3	139	11	09U1A2
35	388.5	59.3	141	11	09U2A5
36	386.5	59.0	118	11	09U2A4
37	386	58.9	117	11	09U2C4
38	384	58.6	157	4	09U5F0
39	381.5	58.2	143	11	09U1V7
40	381.5	58.2	143	11	09U1C4
41	381	58.2	146	11	09U2A8
42	380.5	58.1	143	11	09U2A5
43	380	58.0	144	11	09U2A5
44	380	58.0	484	11	09U1A6
45	379.5	57.9	109	11	09U175

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	124 AA.
09U192	09U192		
AC	09U192		
DT	01-MAY-2000 (TREMBLrel, 13, Created)		
DT	01-MAY-2000 (TREMBLrel, 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION		
DE	(FRAGMENT)		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_Taxid-9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-98277139; PubMed-9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.N.,		
RA	Young D.C.;		
KT	*Myosin-reactive autoantibodies in rheumatic carditis and normal		
KT	fetus.*;		
KT	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL: AF035022; AAD56258.1; -		
DR	HSSP: P01772; 2F84.		
DR	InterPro: IPR003006; 19_MHC.		
DR	InterPro: IPR003596; 19_V.		
DR	Pfam: PF00047; 19_1.		
DR	SMART: SMO0406; IGV; 1.		
FT	NON_TER		
FT	NON_TER		
FT	NON_TER		
SO	SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;		

Query Match 69.8% Score 457.5; DB 4; Length 124;  
Best Local Similarity 69.5% Pred. No. 3.8e-41;  
Matches 91; Conservative 9; Mismatches 16; Indels 15; Gaps 2;  
QY 1 QVQLVSGAEVKKPKASVAVSKASGPNIKDTYTHWFOAGPGRLEMMGRIDPANGTKY 60  
DB 1 EVQLVSGAEVKKPKASVAVSKASGVTFFSYTHWFOAGPGRLEMMGRIDPANGTKY 60

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OY 61 DPKFGQVTTADTSASTAYMELSLRSEDTAVYCCAREGYGNYGYYAM-----DY 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AAKFGQAVTMTREDTSTVYMDLSLRSDEPTAVYYCAR-----GLYVVPAAFSHEDY 113
OY 113 WGGGTAVTVSS 123
      |||||:|||||:
Db 114 WGGGTAVTVSS 124

RESULT 2
ID Q960S0 PRELIMINARY; PRT: 159 AA.
AC Q960S0:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tlison M.D.:
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY039025; AAK82649.1; -.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 67.3%; Score 440.5; DB 4; Length 159;
Best Local Similarity 64.9%; Pred. No. 3.4e-39;
Matches 87; Conservative 13; Mismatches 19; Indels 15; Gaps 2;

OY 1 OVOLVSGAEVKKPGASVKSCAKSGFNKIDTYIHWRQAPGQRLRMGRIDPANGYTRY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 OVOLVSGAEVKKPGASVKSCAKSGFYFSNYYMMWVQAQGGPEMMGVINPSCGSARY 79
OY 61 DPKFGQVTTADTSASTAYMELSLRSEDTAVYYCARE-----GYGNYGYYA 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SOKFGRLMTFRDSTSTVYMDLSLRSDDTAVYFCAREMELTFGGAIVSKGRY---YYG 135
OY 110 MDYWGQGTITVTVSS 123
      |||||:|||||:
Db 136 MDYWGQGTITVTVSS 149

RESULT 3
ID Q99L31 PRELIMINARY; PRT: 468 AA.
AC Q99L31:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.:
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003878; AAH03878.1; -.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003599; 1g_.
DR InterPro: IPR003597; 1g_c1.
DR InterPro: IPR003600; 1g_1like.
DR InterPro: IPR003006; 1g_MHC.
DR InterPro: IPR003596; 1g_v.
DR Pfam: PF00047; 1g; 4.

Query Match 66.0%; Score 432; DB 11; Length 109;
Best Local Similarity 68.7%; Pred. No. 1.7e-38;
Matches 79; Conservative 15; Mismatches 15; Indels 6; Gaps 1;
```

```
DR SMART: SM00409; 1g; 2.
DR SMART: SM00407; 1g_c1; 3.
DR SMART: SM00406; 1g_v; 1.
DR SMART: SM00410; 1g_1like; 1.
DR PROSITE: PS00290; 1g_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 67.2%; Score 440; DB 11; Length 468;
Best Local Similarity 67.5%; Pred. No. 1.5e-38;
Matches 83; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

OY 1 OVOLVSGAEVKKPGASVKSCAKSGFNKIDTYIHWRQAPGQRLRMGRIDPANGYTRY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVOLQSGAEVLPKPGASVKSLCTASGFNIKIDSLHWRQKQPEGLGEMIGMIDPEDETRY 79
OY 61 DPKFGQVTTADTSASTAYMELSLRSEDTAVYCCAREGYGNYGYYAMDYWGQGTITV 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 APRFQDKATITADTSNTAVLQSLTSDEPTAVYCARNLITGCV---YDWGQGTITIT 135
OY 121 VSS 123
      |||
Db 136 VSS 138

RESULT 4
ID Q9UL85 PRELIMINARY; PRT: 109 AA.
AC Q9UL85:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLIOLIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C;
RX MRLINE=20448942; Pubmed=10992488;
RA Markiel S., Liao L., Cunningham M.W., Diamond B.:
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206021; AAF69319.1; -.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; 1g_MHC.
DR InterPro: IPR003596; 1g_v.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g_v; 1.
DR SMART: SM00406; 1g_v; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615F6CED4EDE CRC64;

Query Match 66.0%; Score 432; DB 11; Length 109;
Best Local Similarity 68.7%; Pred. No. 1.7e-38;
Matches 79; Conservative 15; Mismatches 15; Indels 6; Gaps 1;

OY 9 AEVKKPGASVKSCAKSGFNKIDTYIHWRQAPGQRLRMGRIDPANGYTRYDKPFGQRY 68
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AEVLPKPGASVKSLCTASGFNIKIDSLHWRQKQPEGLGEMIGMIDPEDETRY 79
OY 69 TTADTSASTAYMELSLRSEDTAVYCCAREGYGNYGYYAMDYWGQGTITVTVSS 123
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TTSDTSNTAVLQSLTSDEPTAVYCAR-----GAVVFDWGQGTITVTVSS 109

RESULT 5
ID Q9UL94
```

ID	090U94.	PRELIMINARY;	PRT;	119	AA.
AC	090U94.				
DT	01-MAY-2000	(TREMBLrel, 13, Created)			
DT	01-MAY-2000	(TREMBLrel, 13, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel, 13, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).				
DE	Myosin.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98277139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RT	fetus.";				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL: AF035020; AAD56256.1; -.				
DR	HSP: P01810; 2FBJ.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam: PF00047; Ig_1.				
DR	SMART: SM00406; IGV; 1.				
FT	NON_TER	1	119	119	
FT	NON_TER	1	119	119	
SO	SEQUENCE	119	AA;	13205	MM; 13E64F5345FAA16E CRC64;

[illegible]





Db 80 NEKFKGATLTADKSSSTAYVMOSSLTSDSAVYFCARSGY--DYDWA--YMGOGTTLVT 135  
 QY 121 VSS 123  
 Db 136 VSA 138

## RESULT 11

0924R4 PRELIMINARY; PRT; 145 AA.

AC 0924R4; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE V1186.2-D-J-C MU PROTEIN (FRAGMENT)  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067785; BAB63270.1;  
 FT NON\_TER 1  
 FT SEQUENCE 145 AA: 16081 MW; ECDB1A135E05B8AA CRC64;

Query Match 63.4%; Score 415.5; DB 11; Length 145;  
 Best Local Similarity 65.0%; Pred. No. 1.4e-36;  
 Matches 80; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

QY 1 OVOLVSGAEVKKPGASVSKASGFNIKDTYIHWVROAPQGRLEMGRIIDPANGCTYKY 60  
 Db 1 OVOLQOPGAEIVKPGASVSKASGTYFTSYMMHVKRPGRGLEMGRIIDPNSGCTKY 60  
 QY 61 DPKFGGRVITADTSASTAYVMEISLRSEDVAVYCARSGYGNVGYAMYDYGCTTLVT 120  
 Db 61 NEKFKGATLTADKSSSTAYVMOSSLTSDSAVYFCARSDY--DYD-YAMDYMGOGTTLVT 117  
 QY 121 VSS 123  
 Db 118 VSS 120

## RESULT 12

0924R1 PRELIMINARY; PRT; 145 AA.

AC 0924R1; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE V1186.2-D-J-C MU PROTEIN (FRAGMENT)  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067785; BAB63270.1;  
 FT NON\_TER 1

FT NON\_TER 145 145  
 SQ SEQUENCE 145 AA: 15979 MW; 0162DOA26C746C04 CRC64;

Query Match 63.4%; Score 415.5; DB 11; Length 145;  
 Best Local Similarity 64.2%; Pred. No. 1.4e-36;  
 Matches 79; Conservative 16; Mismatches 25; Indels 3; Gaps 1;

QY 1 OVOLVSGAEVKKPGASVSKASGFNIKDTYIHWVROAPQGRLEMGRIIDPANGCTYKY 60  
 Db 1 OVOLQOPGAEIVKPGASVSKASGTYFTSYMMHVKRPGRGLEMGRIIDPNSGCTKY 60  
 QY 61 DPKFGGRVITADTSASTAYVMEISLRSEDVAVYCARSGYGNVGYAMYDYGCTTLVT 120  
 Db 61 NEKFKGATLTADKSSSTAYVMOSSLTSDSAVYFCARSDY--DYD-YAMDYMGOGTTLVT 117  
 QY 121 VSS 123  
 Db 118 VSS 120

## RESULT 13

0924R8 PRELIMINARY; PRT; 146 AA.

AC 0924R8; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE V1186.2-D-J-C MU PROTEIN (FRAGMENT)  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067781; BAB63266.1;  
 FT NON\_TER 1  
 FT SEQUENCE 146 AA: 16216 MW; 92460F1FD1B7538 CRC64;

Query Match 62.9%; Score 412; DB 11; Length 146;  
 Best Local Similarity 63.4%; Pred. No. 3.3e-36;  
 Matches 78; Conservative 19; Mismatches 24; Indels 2; Gaps 2;

QY 1 OVOLVSGAEVKKPGASVSKASGFNIKDTYIHWVROAPQGRLEMGRIIDPANGCTYKY 60  
 Db 1 OVOLQOPGAEIVKPGASVSKASGTYFTSYMMHVKRPGRGLEMGRIIDPNSGCTKY 60  
 QY 61 DPKFGGRVITADTSASTAYVMEISLRSEDVAVYCARSGYGNVGYAMYDYGCTTLVT 120  
 Db 61 NEKFKGATLTADKSSSTAYVMOSSLTSDSAVYFCARSDY--DYD-YAMDYMGOGTTLVT 118  
 QY 121 VSS 123  
 Db 119 VSS 121

## RESULT 14

09UL89 PRELIMINARY; PRT; 116 AA.

AC 09UL89; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION  
 (FRAGMENT).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035025; AAD56261.1; .  
 DR HSSP: P01810; 2FBI.  
 DR InterPro: IPR003006; Iq\_MHC.  
 DR InterPro: IPR003596; Iq\_V.  
 DR Pfam: PF00047; Iq; 1.  
 DR SMART: SM00406; Iq; 1.  
 FT NON\_TER 1  
 FT 116 116  
 SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA98 CRC64;

Query Match 62.8%; Score 411.5; DB 4; Length 116;  
 Best Local Similarity 72.5%; Pred. No. 2.8e-36;  
 Matches 87; Conservative 3; Mismatches 25; Indels 5; Gaps 2;

OY 5 VQSGAEVKKKPGASVSKASGFINIKDTYIHVYRQAPGRLFMNGRIDPANGYTKYDPKF 64  
 DB 1 VQSGAEVKKKPGASVSKASGFINIKDTYIHVYRQAPGRLFMNGRIDPANGYTKYDPKF 60  
 OY 65 QGRVITADTSASTAYMELSLRSEDYAVYYCARREGYGNVGY-AMDYWGQGLTVVSS 123  
 DB 61 QGRVITADTSASTAYMELSLRSEDYAVYYCAS---SNMGPYWYFDLWGRGLTVVSS 116

RESULT 15  
 Q92406 PRELIMINARY; PRT; 145 AA.  
 ID Q92406;  
 AC Q92406;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE VHLB6.2-D-J-C MU PROTEIN (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AB067794; BAB63279.1; .  
 FT NON\_TER 1  
 FT 145 145  
 SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 62.5%; Score 409.5; DB 11; Length 145;  
 Best Local Similarity 63.2%; Pred. No. 6e-36;  
 Matches 79; Conservative 17; Mismatches 22; Indels 7; Gaps 2;

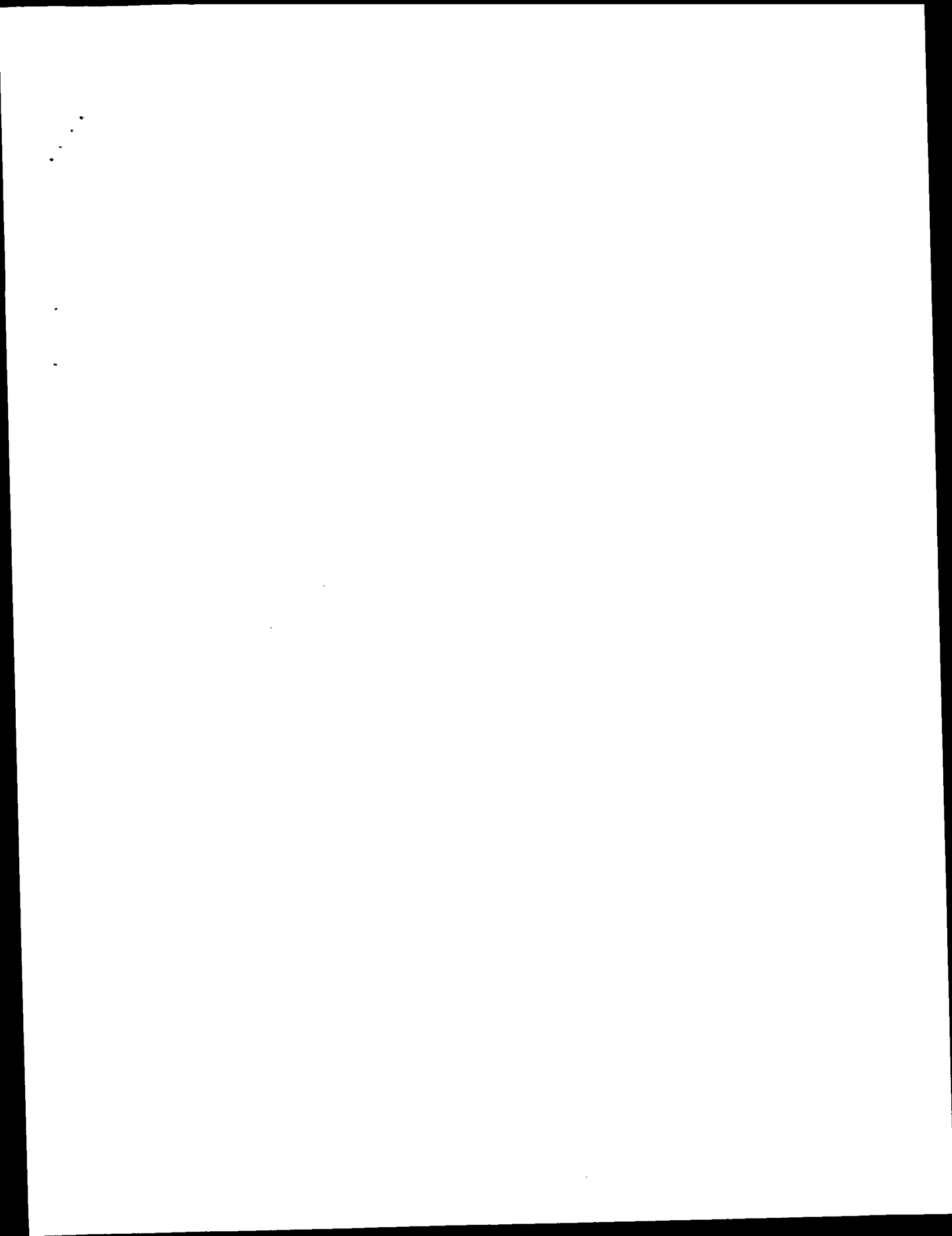
OY 1 OVOLVQSGAEVKKPGASVSKASGFINIKDTYIHVYRQAPGRLFMNGRIDPANGYTKY 60  
 DB 1 OVOLVQSGAEVKKPGASVSKASGFINIKDTYIHVYRQAPGRLFMNGRIDPANGYTKY 60  
 OY 61 DPFQGRVITADTSASTAYMELSLRSEDYAVYYCARREGYGNVGYAMDYWGQGLTV 118  
 DB 61 NEFKSKATLTDKPSSTAYMOLSLTSEDSAVYYCARSTLSHY-----YAMDYWGQGLTS 115

OY 119 VTSS 123  
 DB 116 VTSS 120

Search completed: July 9, 2002, 15:45:36  
 Job time: 387 sec

Tue Jul 9, 15:50:41 2002

us-09-010-377-2.rsp



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 9, 2002, 15:40:36 ; Search time 51.18 Seconds

(without alignments)  
266.942 Million cell updates/sec

Title: US-09-010-377-2

Perfect score: 655  
1 OVALVOSAEFKKPCASVKV.....NYGVYANDYWGQGLTVVSS 123

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	123	16	Humanized VLA-4 an
2	655	100.0	142	16	Human VLA-4 reshap
3	655	100.0	142	18	Humanised alpha-4
4	648	98.9	123	18	Humanised alpha-4
5	552	84.3	123	16	Mouse anti-VLA-4 a
6	544	83.1	140	16	Mouse VLA-4 antibo
7	544	83.1	140	18	Alpha-4 integrin m
8	523.5	79.9	120	19	Heavy chain variat
9	523.5	79.9	136	22	A fusion of single
10	523	79.8	136	16	Human/murine chime
11	523	79.8	136	17	Chimeric human/mu

12	523	79.8	269	16	AA876682	Human ONS-M21 anti
13	523	79.8	269	17	AAW04397	Chimeric human/mu
14	515	78.6	119	16	AA81325	Humanized VLA-4 an
15	515	78.6	119	18	AAW2426	Humanised alpha-4
16	512	78.2	119	16	AA81324	Humanized VLA-4 an
17	512	78.2	119	18	AAW2425	Humanised alpha-4
18	507.5	77.5	135	21	AA807969	A heavy chain vari
19	504.5	77.0	118	14	AA837611	h112R Ab H chain V
20	503	76.8	119	20	AAV52717	Humanised ATR-5 H
21	503	76.8	119	22	AA874978	Humanised ATR-5 H
22	499	76.2	119	20	AAV52719	Humanised ATR-5 H
23	498	76.2	119	22	AA874980	Humanised ATR-5 H
24	496	75.7	136	17	AA892084	Humanised ATR-5 H
25	495	75.6	119	16	AA81331	Humanised ATR-5 H
26	493	75.3	119	20	AAV52718	Humanised ATR-5 H
27	493	75.3	119	22	AA874979	Humanised ATR-5 H
28	492	75.1	117	15	AA857476	Humanised ATR-5 H
29	492	75.1	117	17	AA852079	Humanised ATR-5 H
30	491	75.0	136	15	AA857481	Humanised ATR-5 H
31	491	75.0	119	20	AAV52708	Humanised ATR-5 H
32	491	75.0	119	22	AA874969	Humanised ATR-5 H
33	489.5	74.7	120	18	AAV52720	Humanised ATR-5 H
34	489	74.7	119	20	AAV52721	Humanised ATR-5 H
35	489	74.7	119	22	AA874961	Humanised ATR-5 H
36	487.5	74.4	120	15	AA874961	Humanised ATR-5 H
37	487	74.4	119	20	AAV52712	Humanised ATR-5 H
38	487	74.4	119	22	AAV52715	Humanised ATR-5 H
39	487	74.4	119	22	AA874973	Humanised ATR-5 H
40	487	74.4	119	22	AA874976	Humanised ATR-5 H
41	486	74.2	140	18	AAW21847	Humanised ATR-5 H
42	486	74.2	143	15	AA859942	Humanised heavy ch
43	484.5	74.0	139	14	AA839953	Anti-VLA4 rAb huma
44	484.5	74.0	139	18	AAW29753	gH1 variable dome1
45	484.5	74.0	139	21	AAV56877	gH1 variable dome1

#### ALIGNMENTS

RESULT 1  
AA81323 standard; Protein: 123 AA.  
XX  
AC AA81323:  
XX  
XX 02-APR-1996 (first entry)  
XX  
DE Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.  
XX  
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
XX antibody engineering.  
XX  
OS Mus musculus.  
XX  
PN WO9519790-A1.  
XX  
PD 27-JUL-1995.  
XX  
PE 25-JAN-1995; 95WO-US01219.  
XX  
PR 25-JAN-1994; 94US-0186269.  
XX  
PA (ATHE-) ATHENA NEUROSCIENCES INC.  
XX  
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;  
XX WPL: 1995-269276/35.  
XX  
PT New humanised antibodies against VLA-4 - used for inhibiting  
PT leukocyte adhesion to endothelial cells, partic. for treating  
PT inflammatory disease.  
XX  
PS Claim 11; Page 69; 105pp; English.

XX The sequence encodes the mouse antibody 21.6 heavy chain variable  
 CC region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned  
 CC cDNA sequences of mouse 21.6 VL and VH (AA099889 and AA099892) regions  
 CC are linked to human constant regions in the construction of a humanized  
 CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are  
 CC modified using PCR primers (See AA099895-98) and then subcloned into  
 CC mammalian cell expression vectors containing human kappa or gamma-1  
 CC constant regions. In the humanized light chain, amino acids L45,  
 CC L49, L58 and L69 in the human kappa LC VR framework are replaced  
 CC by the amino acid present in the equivalent position of the mouse  
 CC 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are  
 CC transfected into COS cells. The humanized antibodies can be used  
 CC for inhibiting adhesion of a leukocyte to an endothelial cell and  
 CC for treating inflammatory diseases such as multiple sclerosis. They  
 CC can also be used in the treatment of stroke, cerebral trauma, for  
 CC meningitis or encephalitis. The antibodies can also be used for  
 CC detecting VLA-4, for affinity purification or for generating  
 CC anti-idiotypic antibodies.

XX Sequence 123 AA:

Query Match 100.0%; Score 655; DB 16; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-53;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWQAPGQRLMMGRIDPANGYTRY 60  
 DB 1 GYQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWQAPGQRLMMGRIDPANGYTRY 60  
 OY 61 DKPFGGRVITTDTSASTAYMETLSLRSEDTAVYYCARGGYGNVGYAMDYWGSGTLYT 120  
 DB 61 DKPFGGRVITTDTSASTAYMETLSLRSEDTAVYYCARGGYGNVGYAMDYWGSGTLYT 120  
 OY 121 VSS 123  
 DB 121 VSS 123

RESULT 2  
 AAR81333 standard; Protein; 142 AA.

XX AAR81333;  
 XX 23-MAR-1996 (first entry)  
 XX Human VLA-4 reshaped antibody 21.6 light heavy variable region.  
 DE Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
 KW antibody engineering.  
 XX Homo sapiens.

OS Location/Qualifiers  
 PH 1..19  
 FT /note= "signal peptide"  
 FT 20..49  
 FT /note= "framework region 1"  
 FT 50..54  
 FT /note= "framework region 1"  
 FT 55..68  
 FT /note= "complementarily determining region 1"  
 FT 69..85  
 FT /note= "framework region 2"  
 FT 86..117  
 FT /note= "complementarily determining region 2"  
 FT 118..131  
 FT /note= "framework region 3"  
 FT 132..142  
 FT /note= "complementarily determining region 3"  
 FT /note= "framework region 4"

PN W09519790-A1.

XX 27-JUL-1995.

XX 25-JAN-1995; 95WO-US01219.

XX 25-JAN-1994; 94US-0186269.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Bendig MM, Jones TS, Leger OJ, Saldanha J;

XX WPI: 1995-269276/35.

XX N-PSDB; AA099894.

XX New humanised antibodies against VLA-4 - used for inhibiting

XX leukocyte adhesion to endothelial cells, partic. for treating

XX inflammatory disease.

XX Disclosure; Fig 11; 105pp; English.

XX The sequence represents the human reshaped antibody 21.6 heavy  
 CC chain variable region against leukocyte adhesion molecule VLA-4.  
 CC Cloned cDNA sequences of mouse 21.6 VH (AA099892) and VL (AA099889)  
 CC regions are linked to human constant regions in the construction  
 CC of a humanized antibody against VLA-4. The 5' and 3' ends of the  
 CC mouse cDNAs are modified using PCR primers (AA099895-98) and then  
 CC subcloned into mammalian cell expression vectors containing human  
 CC kappa or gamma-1 constant regions. In the humanized heavy chain,  
 CC amino acids H27, H28, H29, H30, H44 and H71 in the human HC VR  
 CC framework are replaced by the amino acid present in the equivalent  
 CC position of the mouse 21.6 Ig H chain. Plasmids encoding the  
 CC chimeric antibodies are transfected into COS cells. The humanized  
 CC antibodies can be used to inhibit adhesion of a leukocyte to an  
 CC endothelial cell and to treat inflammatory diseases such as multiple  
 CC sclerosis. They can also be used in the treatment of stroke,  
 CC cerebral trauma, meningitis or encephalitis. The antibodies can  
 CC also be used for detecting VLA-4, for affinity purification or for  
 CC generating anti-idiotypic antibodies.

XX Sequence 142 AA:

Query Match 100.0%; Score 655; DB 16; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-53;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWQAPGQRLMMGRIDPANGYTRY 60  
 DB 20 GYQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWQAPGQRLMMGRIDPANGYTRY 79  
 OY 61 DKPFGGRVITTDTSASTAYMETLSLRSEDTAVYYCARGGYGNVGYAMDYWGSGTLYT 120  
 DB 80 DKPFGGRVITTDTSASTAYMETLSLRSEDTAVYYCARGGYGNVGYAMDYWGSGTLYT 139

OY 121 VSS 123  
 DB 140 VSS 142

RESULT 3  
 AAW22428  
 ID AAW22428 standard; Protein; 142 AA.

XX AAW22428;

XX 09-DEC-1997 (first entry)

XX Humanised alpha-4 integrin antibody 21.6 VL version Ha.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;

XX asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;

XX metastasis; inflammatory bowel disease; rheumatoid arthritis;

KW	transplant rejection; graft versus host disease; nephritis;
KM	atopic dermatitis; psoriasis; myocardial ischaemia;
XX	acute leukocyte mediated lung injury; therapy.
OS	Chimeric Mus musculus;
OS	Chimeric Homo sapiens;
XX	Chimeric synthetic.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..19
FT	/label= Leader
FT	20..142
FT	/label= Mac-protein
FT	/note= "VH version Ha (Claim 25)"
FT	20..49
FT	/label= FR1
FT	/note= "21/28/CL framework region 1"
FT	50..55
FT	/label= CDR1
FT	/note= "21.6 complementarity determining region 1"
FT	55..67
FT	/label= FR2
FT	/note= "21/28/CL framework region 2"
FT	68..85
FT	/label= CDR2
FT	/note= "21.6 complementarity determining region 2"
FT	86..117
FT	/label= FR3
FT	/note= "21/28/CL framework region 3"
FT	118..131
FT	/label= CDR3
FT	/note= "21.6 complementarity determining region 3"
FT	132..142
FT	/label= FR4
FT	/note= "21/28/CL framework region 4"
XX	
PN	MO9718838-A1.
PD	23-MAY-1997.
XX	
XX	21-NOV-1996; 96WO-US18807.
XX	
XX	21-NOV-1995; 95US-0561521.
XX	
PA	(ATHE-) ATHENA NEUROSCIENCES INC.
PI	Bendly MM, Jones ST, Leger OJ, Saldanha J, Yednock TA.
XX	WPI: 1997-297879/27.
DR	N-PSDB: AAT74789.
XX	
PS	Example 6; Fig 11; 107pp; English.
XX	
CC	This polypeptide, designated Ha, comprises the heavy chain variable
CC	region (Vh) of a humanised alpha-4 integrin antibody 21.6 (see also
CC	AAW22413). It is composed of complementarity determining regions from
CC	the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC	antibody 21.6 and a modified human 21/28/CL framework. It can be
CC	mutagenised in mammalian host cells following PCR amplification and
CC	humanised 21.6 VH and a humanised 21.6 VJ (see AAW22412) can be used
CC	to produce a claimed humanised 21.6 antibody that is useful in the
CC	manufacture of a medicament for treating asthma, atherosclerosis,
CC	AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC	arthritis, transplant rejection, graft versus host disease, tumour
CC	metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC	ischaemia, and acute leukocyte mediated lung injury. The humanised
CC	antibody has a half-life in the human circulation essentially
CC	equivalent to that of naturally occurring human antibodies.
XX	

Seq	Sequence	142 AA:
Query	Match	100.0%; Score 655; DB 18; Length 142;
	Best Local Similarity	100.0%; Pred. No. 6, 4e-53;
	Matches 123; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1	QVOLVSGAEVKKPKPASVSKVSCASGFIKIDTYIHWVROAPGORLEWGRIPDANGYTRY 60
	20	qqlivqsgaetkkkpgasvskvscasgfnldklylhwvrgpqrlewmgrldpangycky 79
Qy	61	DPKFGRTITADTSASTAYMELSSLESDPTAYVYCARREGYGCNVCVYAMDYWGCGTLYT 120
	80	dptfgvrltadtastaymelsltsedltavycaregyngnyvamydgqglvtc 139
Qy	121	VSS 123
	140	VSS 142
Db	140	VSS 142
RESULT 4		
AAW22413		
ID	AAW22413	standard; Protein; 123 AA.
XX	AAW22413;	
XX	08-DEC-1997	(first entry)
DE	Humanised alpha-4	Integrin antibody 21.6 VH Ha.
KW	Alpha-4	Integrin; humanised antibody; monoclonal antibody 21.6;
KW	acthina; altherosclerosis; AIDS; dementia; diabetes; tumour;	
KW	metastasis; inflammatory bowel disease; rheumatoid arthritis;	
KW	transplant rejection; graft versus host disease; nephritis;	
KW	atopic dermatitis; psoriasis; myocardial ischaemia;	
KW	acute leukocyte mediated lung injury; therapy.	
XX		
OS	Chimeric Mus musculus;	
OS	Chimeric Homo sapiens;	
OS	Chimeric synthetic.	
XX		
XX		
Key	Location/Qualifiers	
FT	1..30	/label= FR1
FT	/note=	"21/28'CL framework region 1"
FT	Misc-difference 27..30	/note=
FT		"21/28'CL residues 27-30 are replaced by
FT		those of Mab 21.6, involved in antigen
FT		binding"
FT	Region	31..35
FT	/label=	CDR1
FT	/note=	"21.6 complementarity determining region 1"
FT	Region	36..49
FT	/label=	FR2
FT	/note=	"21/28'CL framework region 2"
FT	Region	50..66
FT	/label=	CDR2
FT	/note=	"21.6 complementarity determining region 2"
FT	Region	67..98
FT	/label=	FR3
FT	/note=	"21/28'CL framework region 3"
FT	Misc-difference 72	/note=
FT		"21/28'CL Arg-72 is subst. by Ala of mouse
FT		21.6 VL, important in supporting the CDR2
FT	Region	99..112
FT	/label=	CDR3
FT	/note=	"21.6 complementarity determining region 3"
FT	Region	113..123
FT	/label=	FR4
FT	/note=	"21/28'CL framework region 4"
XX		
NN	WO9718838-A1.	

Key	Location/Qualifiers
FT Region	1..30
FT	/label= FR1
FT	/note= "mouse heavy chain variable framework region 1"
FT Region	31..35
FT	/label= CDR1
FT	/note= "mouse heavy chain variable complementarity determining region 1"
FT Region	36..49
FT	/label= FR2
FT	/note= "mouse heavy chain variable framework region 2"
FT Region	50..66
FT	/label= CDR2
FT	/note= "mouse heavy chain variable complementarity determining region 2"
FT Region	67..98
FT	/label= FR3
FT	/note= "mouse heavy chain variable framework region 3"
FT Region	99..112
FT	/label= CDR3
FT	/note= "mouse heavy chain variable complementarity determining region 3"
FT Region	113..123
FT	/label= FR4
FT	/note= "mouse heavy light chain variable framework region 4"
XX	WO9519790-A1.
XX	27-JUL-1995.
XX	25-JAN-1995;
XX	95WO-US01219.
XX	25-JAN-1994;
XX	94US-0186269.
XX	(ATHE-) ATHENA NEUROSCIENCES INC.
XX	Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX	WPI; 1995-269276/35.
PT	New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
PS	Disclosure; Page 68; 105pp; English.
XX	The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the RE1 antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ93895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids 145, 149, 158 and 169 in the human kappa LCVR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into CC cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as cerebral trauma, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotypic antibodies.
XX	Sequence 123 AA;

Query Match 84.3%; Score 552; DB 16; Length 123;



Best Local Similarity 82.9%; Pred. No. 1.7e-43;  
Matches 102; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKKPGASVKYSCKASGFNIKDTYTHWROAPGQRLKMKRIDPANGYTKY 60  
Db 1 evqlqgsgaelvkvpgasvklscasgfnldklythcvkqrpqglawlgfripangytky 60  
QY 61 DPKFGCVITTAQTSASTAVAMELSSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 120  
Db 61 dprfggkaltladsntaylqlssltseclayfcaregyngyngvamydwgqglavt 120  
QY 121 VSS 123  
Db 121 vsa 123

## RESULT 6

AA081327  
ID AAR01327 standard; Protein; 140 AA.

AC AAR01327;  
DT 23-MAR-1996 (first entry)  
DE Mouse VLA-4 antibody 21.6 light heavy variable region.  
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
KW antibody engineering.  
OS Mus musculus.

FT Key Location/Qualifiers  
FT Peptide 1..19  
FT Region /note= "signal peptide"  
FT Region 20..49  
FT Region /note= "framework region 1"  
FT Region 50..54  
FT Region /note= "complementarity determining region 1"  
FT Region 55..68  
FT Region /note= "framework region 2"  
FT Region 69..85  
FT Region /note= "complementarity determining region 2"  
FT Region 86..117  
FT Region /note= "framework region 3"  
FT Region 118..131  
FT Region /note= "complementarity determining region 3"  
FT Region 132..140  
FT /note= "framework region 4"

MO9519790-A1.

27-JUL-1995.

25-JAN-1995; 95MO-US01219.

25-JAN-1994; 94US-0186269.

(ATHE-) ATHENA NEUROSCIENCES INC.

Bendig MM, Jones TS, Leger OJ, Saldanha J;

WPI; 1995-269276/35.

N-PSDB; AA099892.

New humanised antibodies against VLA-4 - used for inhibiting  
leukocyte adhesion to endothelial cells, partic. for treating  
inflammatory disease.

Disclosure: Fig 2; 105pp; English.

The sequence represents the mouse antibody 21.6 heavy chain variable  
region directed against leukocyte adhesion molecule VLA-4. Cloned  
cDNA sequences of mouse 21.6 VH and VL (see AA099892) regions are

CC linked to human constant regions in the construction of a humanized  
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are  
CC modified using PCR primers (See AA099895-98) and then subcloned into  
CC mammalian cell expression vectors containing human kappa or gamma-1  
CC constant regions. In the humanized heavy chain, amino acids H27,  
CC H28, H29, H30, H44 and H71 in the human HC VR framework are replaced  
CC by the amino acid present in the equivalent position of the mouse  
CC transfectant into COS cells. The humanized antibodies are  
CC to inhibit adhesion of a leukocyte to an endothelial cell and  
CC can also be used in the treatment of stroke, cerebral traumas,  
CC meningitis or encephalitis. The antibodies can also be used for  
CC detecting VLA-4, for affinity purification or for generating  
CC anti-idiotypic antibodies.

Sequence 140 AA;

Query Match  
Best Local Similarity 83.1%; Score 544; DB 16; Length 140;  
Matches 100; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKKPGASVKYSCKASGFNIKDTYTHWROAPGQRLKMKRIDPANGYTKY 60  
Db 20 evqlqgsgaelvkvpgasvklscasgfnldklythcvkqrpqglawlgfripangytky 79  
QY 61 DPKFGCVITTAQTSASTAVAMELSSLRSEDTAVYVCAREGYGNGVYAMDYWGCGTLVT 120  
Db 80 dprfggkaltladsntaylqlssltseclayfcaregyngyngvamydwgqglavt 139  
QY 121 V 121  
Db 140 v 140

## RESULT 7

AAW22410  
ID AAW22410 standard; Protein; 140 AA.

AAW22410;

DT 08-DEC-1997 (first entry)

DE Alpha-4 integrin mouse MAB 21.6 VH region.

KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;  
KW metastasis; inflammatory bowel disease; rheumatoid arthritis;  
KW transplant rejection; graft versus host disease; nephritis;  
KW atopic dermatitis; psoriasis; myocardial ischaemia;  
KW acute leukocyte mediated lung injury; therapy.

Mus musculus.

FT Key Location/Qualifiers  
FT Peptide 1..19  
FT Region /label= Leader  
FT Region 20..49  
FT Region /label= FR1  
FT Region /note= "framework region 1"  
FT Region 50..54  
FT Region /label= CDR1  
FT Region /note= "complementarity determining region 1"  
FT Region 55..68  
FT Region /label= FR2  
FT Region /note= "framework region 2"  
FT Region 69..85  
FT Region /label= CDR2  
FT Region /note= "complementarity determining region 2"  
FT Region 86..117  
FT Region /label= FR3  
FT /note= "framework region 3"



XX A fusion of single chain antibody/streptavidin.  
DE AAR76681 standard; protein; 136 AA.

XX Streptavidin: tumour cell; cancer; adenocarcinoma;  
KM hematology; malignancy; humn-LU-10; EGP40; EPCAM.

XX Synthetic.  
OS Streptomyces avidin11.

XX Homo sapiens.  
PN WO200075333-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000MO-US15595.

XX 07-JUN-1999; 99US-0137900.

XX 03-DEC-1999; 99US-0168976.

XX (NEOR-) NEORX CORP.

XX Goshorn SC, Graves SS, Schultz JB, Lin Y, Sanderson JA, Reno JM;  
DR WPI: 2001-091213/10.

XX N-PSDB; AAC86562.

XX New vector constructs for expressing genomic streptavidin fusion  
PT proteins which are useful for targeting tumour cells associated with  
PT cancer, e.g. adenocarcinomas.

XX Example 1; Fig 10; 100pp; English.

XX The present sequence encodes a fusion of the single chain antibody  
CC humn-LU-10 and streptavidin. The antibody binds the antigen EGP40 or  
CC EPCAM. The fusion protein is expressed using vectors of the invention.  
CC The specification describes vector constructs for expressing streptavidin  
CC fusion proteins. The vector comprises a first nucleic acid encoding  
CC streptavidin or its functional variant operatively linked to a promoter,  
CC and a cloning site for insertion of a second nucleic acid sequence  
CC encoding a polypeptide to be fused with streptavidin, interposed between  
CC the promoter and the first nucleic acid sequence. Alternatively, the  
CC vector construct comprises a first nucleic acid operatively linked to a  
CC promoter, encoding a polypeptide to be fused with streptavidin, and a  
CC cloning site for insertion of a second nucleic acid encoding at least  
CC 129 amino acids of streptavidin or its functional variant. The fusion  
CC proteins are useful for targeting tumour cells, particularly tumour cells  
CC associated with cancer, e.g. adenocarcinomas or hematological  
CC malignancies. The vector construct is useful for expressing of  
CC streptavidin fusion proteins. In particular, these are useful as tools  
CC for medical diagnostics and therapeutic purposes, e.g. for detecting the  
CC presence or absence of, or treating, a target site within a mammalian  
CC host.

XX Sequence 431 AA:

Query Match 79.9%: Score 523.5; DB 22; Length 431;  
Best Local Similarity 82.9%: Pred. No. 2,8e-40;  
Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVOLVQSGAEVKKPKGASVSKASGFIKDTYTHWVROAPGRLWEMGRIDPANGYTKY 60

DB 148 qvqlvqsgaevkpkgsavkscasgfnlkdlyhwvrgpqqglwmgrldpangntks 207

QY 61 DKPFGGRVTTADTSASTAYMELSSLRSEDPNAVYYCARREGYGYGVYANDWYCOGTLVT 120

DB 208 dlsfggrvltadtsastaymelslrseddnavyycesrevl---tgkwsldywgqglvtl 264

QY 121 VSS 123

DB 265 vas 267

RESULT 10

AA76681

1D AAR76681 standard; protein; 136 AA.

XX AAR76681;

XX 17-JAN-1996 (first entry)

XX Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.

XX Human: murine; chimeric antibody; HEF-RVL-M21g(gamma)1;

XX medulloblastoma; brain tumour; treatment; diagnosis.

XX Homo sapiens.

XX Key

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

XX Peptide

Query Match 79.8%: Score 523; DB 16; Length 136;  
Best Local Similarity 83.7%: Pred. No. 8,8e-41;  
Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps 2;

QY 1 QVOLVQSGAEVKKPKGASVSKASGFIKDTYTHWVROAPGRLWEMGRIDPANGYTKY 60

DB 20 qvqlvqsgaevkpkgsavkscasgfnlkdlyhwvrgpqqglwmgrldpangntks 79

QY 61 DKPFGGRVTTADTSASTAYMELSSLRSEDPNAVYYCARREGYGYGVYANDWYCOGTLVT 120

DB 80 dpkfggrvltadtsastaymelslrseddnavyycesrevl---gdvqgglvtl 133

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267

QY 121 VSS 123

DB 265 vas 267



Query Match 79.8%; Score 523; DB 16; Length 269;  
 Best Local Similarity 83.7%; Pred. No. 1,9e-40;  
 Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps 2;

OY 1 OVOLVSGAEVKKPGASVSKASGKFNKDTYIHVWRQAPGRLWMGRIDPANGYTKY 60  
 Db 23 qvqlvsgaeavkpgssvskasgfnldtlylhvwrqapggqlemgrldpadgnlky 82

OY 61 DPKFGQVTTTADTSASTAYMELSLRSEDTAVYYCARREGYGCYVAMDYWGCTLVLT 120  
 Db 83 dpkfgqrvtltadesntntaymelslrsestdafyica-sayvvn----qdywqgqlvt 136

OY 121 VSS 123  
 |||  
 Db 137 VSS 139

RESULT 13  
 AAW04397 standard; Protein: 269 AA.

AC AAW04397;  
 XX  
 XX 09-DEC-1996 (first entry)  
 DE Chimeric human/murine MAb ONS-M21 scfv fragment.  
 XX  
 KM Murine; human; myeloblastoma; chimaera; monoclonal antibody;  
 KM chimeric single stranded fv region; low human antigenicity;  
 KW diagnosis; treatment; cerebral tumour; reshaped.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= sig-peptide  
 FT Region 23..139  
 FT /note= "heavy variable region"  
 FT Peptide 140..154  
 FT /label= linker  
 FT Region 155..261  
 FT /note= "light variable region"  
 FT Peptide 262..269  
 FT /label= FLAG

XX  
 PN JP08169900-A.  
 XX  
 PD 02-JUL-1996.  
 XX  
 PF 18-NOV-1994; 94JP-0285057.  
 XX  
 PR 18-OCT-1994; 94JP-0252166.  
 PR 19-NOV-1993; 93JP-0291078.  
 XX  
 PA (CHUS) CHUGAI PHARM CO LTD.  
 XX  
 DR WPI: 1996-358509/36.  
 DR N-PSDB: AAT38662.  
 XX  
 PT Reshaped anti-human myeloblastoma cell human antibody - has low  
 PT human antigenicity, and is therefore useful for diagnosis and  
 PT treatment of cerebral tumours, e.g. myeloblastoma  
 XX  
 PS Example 6; Pages 40-41; 45pp; Japanese.

CC The present sequence is a scfv fragment from the chimaeric  
 CC human/murine monoclonal antibody (MAb) ONS-M21. The MAb was  
 CC prep'd. by combining light and heavy variable region DNA, from a  
 CC murine anti-human myeloblastoma cell MAb, with human light and  
 CC heavy constant region sequences, respectively to produce chimeric  
 CC human/murine light and heavy chain DNA mols.. A recombinant vector  
 CC for the expression of the heavy and light chain DNA mols. was

CC prep'd., and used to transform a host cell. The host cell was then  
 CC cultured, and the expression prods. of the heavy and light chain  
 CC DNA mols. sepd. and connected with a peptide linker to produce a  
 CC single stranded fv region. The reshaped fv region has low human  
 CC antigenicity, and is therefore expected to be useful as an agent  
 CC for the diagnosis and treatment of cerebral tumours,  
 CC e.g. myeloblastoma.  
 XX  
 SO Sequence 269 AA.

Query Match 79.8%; Score 523; DB 17; Length 269;  
 Best Local Similarity 83.7%; Pred. No. 1,9e-40;  
 Matches 103; Conservative 4; Mismatches 10; Indels 6; Gaps 2;

OY 1 OVOLVSGAEVKKPGASVSKASGKFNKDTYIHVWRQAPGRLWMGRIDPANGYTKY 60  
 Db 23 qvqlvsgaeavkpgssvskasgfnldtlylhvwrqapggqlemgrldpadgnlky 82

OY 61 DPKFGQVTTTADTSASTAYMELSLRSEDTAVYYCARREGYGCYVAMDYWGCTLVLT 120  
 Db 83 dpkfgqrvtltadesntntaymelslrsestdafyica-sayvvn----qdywqgqlvt 136

OY 121 VSS 123  
 |||  
 Db 137 VSS 139

RESULT 14  
 AAR81325 standard; Protein: 119 AA.

ID AAR81325;  
 AC AAR81325;  
 XX  
 XX 02-APR-1996 (first entry)  
 DE Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.  
 XX  
 XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;  
 KW antibody engineering.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09519790-A1.  
 XX  
 PD 27-JUL-1995.  
 XX  
 PF 25-JAN-1995; 95MO-US01219.  
 XX  
 PR 25-JAN-1994; 94US-0186269.  
 XX  
 PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 XX  
 PI Bendig MM, Jones TS, Leger OJ, Saldanha J;  
 XX  
 DR WPI: 1995-269276/35.  
 DR  
 XX  
 PT New humanised antibodies against VLA-4 - used for inhibiting  
 PT leukocyte adhesion to endothelial cells, partic. for treating  
 PT inflammatory disease.  
 XX  
 PS Claim 13; Page 70; 105pp; English.

CC The sequence encodes the mouse antibody 21.6 heavy chain variable  
 CC region, Hc, directed against leukocyte adhesion molecule VLA-4. Cloned  
 CC cDNA sequences of mouse 21.6 VL and VH (AA09889 and AA09892) regions  
 CC are linked to human constant regions in the construction of a humanized  
 CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are  
 CC modified using PCR primers (See AA09895-98) and then subcloned into  
 CC mammalian cell expression vectors containing human Kappa or gamma-1  
 CC constant regions. In the humanized light chain, amino acids 145,  
 CC 149, 158 and 169 in the human kappa LC VR framework are replaced  
 CC by the amino acid present in the equivalent position of the mouse

CC 21.6 Ig L chain. plasmids encoding the chimeric antibodies are  
 CC transfected into COS cells. The humanized antibodies can be used  
 CC for inhibiting adhesion of a leukocyte to an endothelial cell and  
 CC for treating inflammatory diseases such as multiple sclerosis. They  
 CC can also be used in the treatment of stroke, cerebral traumas,  
 CC meningitis or encephalitis. The antibodies can also be used for  
 CC detecting VLA-4, for affinity purification or for generating  
 CC anti-idiotypic antibodies.

XX Sequence 119 AA:

Query Match 78.6%; Score 515; DB 16; Length 119;  
 Best Local Similarity 82.9%; Pred. No. 4.1e-40;  
 Matches 102; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

OY 1 OYOLVSGAEVKKPGASVKASKASGFNFKDITYIHVWRQAPGQRLMKGRIDPANGYTRY 60  
 DB 1 qvqlvsgaevkpkpgasvskaskasgfinksyamhwvraqpgrlemwmgwinaqgnky 60  
 OY 61 DPKFGQRTTADTSASTAYMELSLKSEDTAVYYCARBEGYNGYVAMDYWGQGLTVT 120  
 DB 61 sgklfgqvltladsastaymelslrsedcavyycaargyfgs----gsnywgqglvt 116  
 OY 121 VSS 123  
 DB 117 VSS 119

# RESULT 15

AAW22426  
 ID AAW22426 standard; Protein: 119 AA.

XX AAW22426;

XX 09-DEC-1997 (first entry)

XX Humanised alpha-4 integrin antibody 21.6 VH Hc.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
 XX asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;  
 XX metastasis; inflammatory bowel disease; rheumatoid arthritis;  
 XX transplant rejection; graft versus host disease; nephritis;  
 XX atopic dermatitis; psoriasis; myocardial ischaemia;  
 XX acute leukocyte mediated lung injury; therapy.

XX Chimeric Mus musculus;  
 OS Chimeric Homo sapiens;  
 OS Chimeric synthetic.

XX Key Location/Qualifiers  
 XX 1..30  
 XX /label= FR1  
 XX /note= "21/28/CL framework region 1"

XX Misc-difference 27..30  
 XX /note= "21/28/CL residues 27-30 are replaced by  
 XX those of Mab 21.6, involved in antigen  
 XX binding"

XX Region 31..35  
 XX /label= CDR1  
 XX /note= "21.6 complementarity determining region 1"

XX Region 36..49  
 XX /label= FR2  
 XX /note= "21/28/CL framework region 2"

XX Region 50..66  
 XX /label= CDR2  
 XX /note= "21.6 complementarity determining region 2"

XX Region 67..98  
 XX /label= FR3  
 XX /note= "21/28/CL framework region 3"

XX Misc-difference 72  
 XX /note= "21/28/CL Arg-72 is substd. by Ala of mouse  
 XX 21.6 VL, important in supporting the CDR2

FT Region 99..112  
 FT /label= CDR3  
 FT /note= "21.6 complementarity determining region 3"  
 FT Misc-difference 102  
 FT /note= "21/28/CL Tyr-102 is substd. by Phe of human  
 FT VCAM-1"  
 FT Region 113..123  
 FT /label= FR4  
 FT /note= "21/28/CL framework region 4"

PN WO9718838-A1.

PD 29-MAY-1997.

PE 21-NOV-1996; 96WO-US18807.

PR 21-NOV-1995; 95US-0561521.

PA (ATHE-) ATHENA NEUROSCIENCES INC.

PI Bending MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;

XX WPI; 1997-297879/27.

PT Uses of humanised alpha-4 integrin antibody - for treatment of  
 PT asthma, atherosclerosis, AIDS, dementia, etc.

XX Example 5; Fig 7; 107pp; English.

XX This polypeptide, designated Hc, comprises the heavy chain variable  
 XX region (VH) of a humanised alpha-4 integrin antibody 21.6. It is  
 XX composed of complementarity determining regions (CDRs) from the VH  
 XX region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody  
 XX 21.6 and a modified human 21/28/CL framework. It contains an  
 XX additional amino acid substitution (Tyr102Phe) in comparison to  
 XX claimed humanised 21.6 VH version Ha (see AAW22412). Humanised  
 XX 21.6 VH and VL regions are used to produce claimed humanised 21.6  
 XX antibodies useful in the manufacture of a medicament for treating  
 XX CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory  
 XX CC bowel disease, rheumatoid arthritis, transplant rejection, graft  
 XX CC versus host disease, tumour metastasis, nephritis, atopic  
 XX CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte  
 XX CC mediated lung injury. The humanised antibodies have a half-life  
 XX in the human circulation essentially equivalent to that of  
 XX naturally occurring human antibodies.

XX Sequence 119 AA:

Query Match 78.6%; Score 515; DB 16; Length 119;  
 Best Local Similarity 82.9%; Pred. No. 4.1e-40;  
 Matches 102; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

OY 1 OYOLVSGAEVKKPGASVKASKASGFNFKDITYIHVWRQAPGQRLMKGRIDPANGYTRY 60  
 DB 1 qvqlvsgaevkpkpgasvskaskasgfinksyamhwvraqpgrlemwmgwinaqgnky 60

OY 61 DPKFGQRTTADTSASTAYMELSLKSEDTAVYYCARBEGYNGYVAMDYWGQGLTVT 120  
 DB 61 sgklfgqvltladsastaymelslrsedcavyycaargyfgs----gsnywgqglvt 116

OY 121 VSS 123  
 DB 117 VSS 119

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Tue Jul 9 15:50:36 2002

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